

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: April 17, 2006, 23:57:18 ; Search time 363 Seconds  
(without alignments)  
1475.762 Million cell updates/sec

Title: US-10-663-241-32

Perfect score: 133  
Sequence: 1 gtcctccgcgcgtcgtctcaaa.....tacagttgtagggaggatt 133

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 9281099 seqs, 2013915447 residues

Total number of hits satisfying chosen parameters: 18562198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications NA\_New:\*  
1: /SIDS5/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
2: /SIDS5/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
3: /SIDS5/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
4: /SIDS5/ptodata/1/pubpna/PCIT\_NEW\_PUB.seq:\*  
5: /SIDS5/ptodata/1/pubpna/US05\_NEW\_PUB.seq:\*  
6: /SIDS5/ptodata/1/pubpna/US02\_NEW\_PUB.seq:\*  
7: /SIDS5/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
8: /SIDS5/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
9: /SIDS5/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
10: /SIDS5/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
11: /SIDS5/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
12: /SIDS5/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
13: /SIDS5/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
14: /SIDS5/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
15: /SIDS5/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	122	91.7	176	9	US-10-527-048-14
2	122	91.7	5834	9	US-10-527-048-15
3	122	91.7	6465	9	US-10-527-048-25
4	122	91.7	6659	9	US-10-527-048-22
5	122	91.7	7549	9	US-10-527-048-24
6	102.8	77.3	2569	11	US-11-190-122-3
7	102.8	77.3	2800	11	US-11-190-122-1
8	102.8	77.3	3119	11	US-11-190-122-2
9	62.2	46.8	8040	11	US-11-004-399-377
10	62.2	46.8	8082	11	US-11-004-399-378
11	62.2	46.8	8082	11	US-11-004-399-483
12	62.2	46.8	8082	11	US-11-004-399-605
13	62.2	46.8	9348	11	US-11-004-399-1
14	62.2	46.8	9348	11	US-11-004-399-113
15	62.2	46.8	9348	11	US-11-004-399-274
16	62.2	46.8	10591	11	US-11-004-399-3593
17	62.2	46.8	10591	11	US-11-004-399-3738
18	62.2	46.8	10591	11	US-11-004-399-3916

C	19	29.4	22.1	9136	14	US-11-136-527-3808	Sequence 3808, Ap
C	20	29	21.8	7479	14	US-11-136-527-3308	Sequence 3308, Ap
C	21	27.6	20.8	507	6	US-09-925-065A-132558	Sequence 132558, Ap
C	22	27.6	20.8	507	6	US-09-925-065A-132559	Sequence 132559, Ap
C	23	27.6	20.8	507	6	US-09-925-065A-132560	Sequence 132560, Ap
C	24	27.6	20.8	518	9	US-10-301-480-284	Sequence 284, App
C	25	27.6	20.8	518	10	US-10-301-480-613693	Sequence 613693, Ap
C	26	27.6	20.8	526	10	US-10-301-480-228769	Sequence 228769, Ap
C	27	27.6	20.8	526	10	US-10-301-480-228770	Sequence 228770, Ap
C	28	27.6	20.8	526	10	US-10-301-480-228771	Sequence 228771, Ap
C	29	27.6	20.8	526	10	US-10-301-480-842178	Sequence 842178, Ap
C	30	27.6	20.8	526	10	US-10-301-480-842179	Sequence 842179, Ap
C	31	27.6	20.8	526	10	US-10-301-480-842180	Sequence 842180, Ap
C	32	27.6	20.8	1095	6	US-09-925-065A-698990	Sequence 698990, Ap
C	33	27.4	20.6	640	6	US-09-925-065A-512538	Sequence 512538, Ap
C	34	27.4	20.6	61487	14	US-11-124-3678-5103	Sequence 5103, Ap
C	35	27.2	20.5	634	9	US-10-301-480-26304	Sequence 26304, A
C	36	27.2	20.5	634	9	US-10-301-480-26305	Sequence 26305, A
C	37	27.2	20.5	634	10	US-10-301-480-639713	Sequence 639713, A
C	38	27.2	20.5	634	10	US-10-301-480-639714	Sequence 639714, A
C	39	27	20.3	533	6	US-09-925-065A-13188	Sequence 13188, A
C	40	27	20.3	533	9	US-10-301-480-114425	Sequence 114425, A
C	41	27	20.3	533	10	US-10-301-480-727834	Sequence 727834, A
C	42	27	20.3	568	6	US-09-925-065A-619601	Sequence 619601, Ap
C	43	27	20.3	985	14	US-11-136-527-1708	Sequence 1708, Ap
C	44	27	20.3	985	14	US-11-136-527-5804	Sequence 5804, Ap
C	45	27	20.3	1694969	7	US-10-506-454-1690	Sequence 1690, Ap

# ALIGNMENTS

RESULT 1  
US-10-527-048-14  
Sequence 14, Application US/10527048  
Publication No. US20060267041  
GENERAL INFORMATION:  
APPLICANT: Center for Genetic Engineering and Biotechnology.  
TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOPERM TRANSPLASTOMIC PLANTS.  
FILE REFERENCE: Vector for plasmid transformation  
CURRENT APPLICATION NUMBER: US/10/527,048  
CURRENT FILING DATE: 2005-03-07  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 14  
LENGTH: 176  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA  
OTHER INFORMATION: fragment codifying for the promoter region of the plasmid 16S  
US-10-527-048-14  
US-10-527-048-14

Query Match 91.7%; Score 122; DB 9; Length 176;

Best Local Similarity 99.3%; Pred. No. 8.1e-11;

Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY	1	GCTCCCCCGCGCTGTTCAATGATGATGATTAAGAGCTGTGGATTGACGTAGGGG	60
DB	16	GCTCCCCCGCGCTGTTCAATGATGATGATTAAGAGCTGTGGATTGACGTAGGGG	75
QY	61	CAGGATGAGTAA-TTCTGGAGGAGCACTCGGGGGAATACGAAGCGCTTGATCACT	119
DB	76	CAGGATGAGTAA-TTCTGGAGGAGCACTCGGGGGAATACGAAGCGCTTGATCACT	135
QY	120	TGTAGGAGGAGATT	133
DB	136	TGTAGGAGGAGATT	149

RESULT 2  
US-10-527-048-15

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/ Sequence 15, Application US/10527048
/ Publication No. US20060026704A1
/ GENERAL INFORMATION:
/ APPLICANT: Center for Genetic Engineering and Biotechnology.
/ TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.
/ FILE REFERENCE: Vector for plasmid transformation
/ CURRENT APPLICATION NUMBER: US/10/527,048
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 15
/ LENGTH: 5834
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DNA
/ OTHER INFORMATION: fragment from the vector pYTPA between the rice atpB and
/ OTHER INFORMATION: tobacco rbcL borders.
US-10-527-048-15
```

```
Query Match          91.7%; Score 122; DB 9; Length 5834;
Best Local Similarity 99.3%; Pred. No. 1.5e-30;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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QY 1 GCTCCCCCGCGTCTTCATAGATGAGTAAAGAGGCTCTGTGGATTGACGTGAGGGG 60
DB 1918 GCTCCCCCGCGTCTTCATAGATGAGTAAAGAGGCTCTGTGGATTGACGTGAGGGG 1977
QY 61 CAGGATGGCTATA-TTCTGGAGGCGAAGCTCCGGGGAATACGACCGCTTGATACAGT 119
DB 1978 CAGGATGGCTATAATTCTGGAGGCGAAGCTCCGGGGAATACGACCGCTTGATACAGT 2037
QY 120 TGTAGGAGGAGATT 133
DB 2038 TGTAGGAGGAGATT 2051
```

```
RESU 3
US-10-527-048-25
```

```
/ Sequence 25, Application US/10527048
/ Publication No. US20060026704A1
/ GENERAL INFORMATION:
/ APPLICANT: Center for Genetic Engineering and Biotechnology.
/ TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.
/ FILE REFERENCE: Vector for plasmid transformation
/ CURRENT APPLICATION NUMBER: US/10/527,048
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 25
/ LENGTH: 6465
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DNA
/ OTHER INFORMATION: fragment from the vector pYTPA-Bar between the rice atpB and
/ OTHER INFORMATION: tobacco rbcL borders.
US-10-527-048-25
```

```
Query Match          91.7%; Score 122; DB 9; Length 6465;
Best Local Similarity 99.3%; Pred. No. 1.5e-30;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGTCTTCATAGATGAGTAAAGAGGCTCTGTGGATTGACGTGAGGGG 60
DB 1918 GCTCCCCCGCGTCTTCATAGATGAGTAAAGAGGCTCTGTGGATTGACGTGAGGGG 1977
QY 61 CAGGATGGCTATA-TTCTGGAGGCGAAGCTCCGGGGAATACGACCGCTTGATACAGT 119
DB 1978 CAGGATGGCTATAATTCTGGAGGCGAAGCTCCGGGGAATACGACCGCTTGATACAGT 2037
QY 120 TGTAGGAGGAGATT 133
```

```
DB 2038 TGTAGGAGGAGATT 2051
```

```
RESULT 4
US-10-527-048-22
/ Sequence 22, Application US/10527048
/ Publication No. US20060026704A1
/ GENERAL INFORMATION:
/ APPLICANT: Center for Genetic Engineering and Biotechnology.
/ TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.
/ FILE REFERENCE: Vector for plasmid transformation
/ CURRENT APPLICATION NUMBER: US/10/527,048
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 22
/ LENGTH: 6659
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DNA
/ OTHER INFORMATION: fragment from the vector pYTPA-aada between the rice atpB and
/ OTHER INFORMATION: tobacco rbcL borders.
US-10-527-048-22
```

```
Query Match          91.7%; Score 122; DB 9; Length 6659;
Best Local Similarity 99.3%; Pred. No. 1.5e-30;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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```
QY 1 GCTCCCCCGCGTCTTCATAGATGAGTAAAGAGGCTCTGTGGATTGACGTGAGGGG 60
DB 1918 GCTCCCCCGCGTCTTCATAGATGAGTAAAGAGGCTCTGTGGATTGACGTGAGGGG 1977
QY 61 CAGGATGGCTATA-TTCTGGAGGCGAAGCTCCGGGGAATACGACCGCTTGATACAGT 119
DB 1978 CAGGATGGCTATAATTCTGGAGGCGAAGCTCCGGGGAATACGACCGCTTGATACAGT 2037
QY 120 TGTAGGAGGAGATT 133
DB 2038 TGTAGGAGGAGATT 2051
```

```
RESULT 5
US-10-527-048-24
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```
/ Sequence 24, Application US/10527048
/ Publication No. US20060026704A1
/ GENERAL INFORMATION:
/ APPLICANT: Center for Genetic Engineering and Biotechnology.
/ TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.
/ FILE REFERENCE: Vector for plasmid transformation
/ CURRENT APPLICATION NUMBER: US/10/527,048
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 24
/ LENGTH: 7549
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DNA
/ OTHER INFORMATION: fragment from the vector pYTPA-HB-aada between the rice atpB and
/ OTHER INFORMATION: tobacco rbcL borders.
US-10-527-048-24
```

```
Query Match          91.7%; Score 122; DB 9; Length 7549;
Best Local Similarity 99.3%; Pred. No. 1.6e-30;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGTCTTCATAGATGAGTAAAGAGGCTCTGTGGATTGACGTGAGGGG 60
DB 2808 GCTCCCCCGCGTCTTCATAGATGAGTAAAGAGGCTCTGTGGATTGACGTGAGGGG 2867
QY 61 CAGGATGGCTATA-TTCTGGAGGCGAAGCTCCGGGGAATACGACCGCTTGATACAGT 119
```

Db 2868 CAGGATGCTATATTTCTGGAGCGAATCCGGCGAATGCAAGCGCTTGATACGT 2927  
QY 120 TGTAGGAGGAGATT 133  
Db 2928 TGTAGGAGGAGATT 2941

## RESULT 6

US-11-190-122-3  
; Sequence 3, Application US/11190122  
; Publication No. US20060031964A1  
; GENERAL INFORMATION:  
; APPLICANT: Daniell, Henry  
; TITLE OF INVENTION: Placid Genetic Engineering Via Somatic Embryogenesis  
; FILE REFERENCE: CHL-T107C322  
; CURRENT APPLICATION NUMBER: US/11/190,122  
; CURRENT FILING DATE: 2005-07-25  
; PRIOR APPLICATION NUMBER: 60/344,704  
; PRIOR FILING DATE: 2001-12-26  
; PRIOR APPLICATION NUMBER: 10/500,351  
; PRIOR FILING DATE: 2004-06-25  
; PRIOR APPLICATION NUMBER: pct/us2003/021157  
; PRIOR FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: 60/590,848  
; PRIOR FILING DATE: 2004-07-23  
; PRIOR APPLICATION NUMBER: 60/590,751  
; PRIOR FILING DATE: 2004-07-23  
; PRIOR APPLICATION NUMBER: 10/519,821  
; PRIOR FILING DATE: 2004-12-30  
; PRIOR APPLICATION NUMBER: 60/400,816  
; PRIOR FILING DATE: 2002-08-02  
; PRIOR APPLICATION NUMBER: 60/393,651  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: 60/393,428  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: PCT/US2002/041503  
; PRIOR FILING DATE: 2002-12-26  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 2569  
; TYPE: DNA  
; ORGANISM: ARTIFICIAL  
; FEATURE:  
; OTHER INFORMATION: alpha-6/nptII expression cassette  
US-11-190-122-3

Query Match 77.3%; Score 102.8; DB 11; Length 2569;  
Best Local Similarity 90.3%; Pred. No. 3.1e-24;  
Matches 121; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGCTTCATAGAGATGATAGAGGCTGTGGATTGACGTGAGGGG 60  
Db 79 GCTCCCCCGCGCTTCATAGAGATGATAGAGGCTGTGGATTGACGTGAGGGG 138  
QY 61 CAGGATGCTATATTTCTGGAGCGAATCCGGCGAATGCAAGCGCTTGATACGT 119  
Db 139 CAGGATGCTATATTTCTGGAGCGAATCCGGCGAATGCAAGCGCTTGATACG 198  
QY 120 TGTAGGAGGAGATT 133  
Db 199 TGTAGGAGGAGATT 212

## RESULT 7

US-11-190-122-1  
; Sequence 1, Application US/11190122  
; Publication No. US20060031964A1  
; GENERAL INFORMATION:  
; APPLICANT: Daniell, Henry  
; TITLE OF INVENTION: Placid Genetic Engineering Via Somatic Embryogenesis  
; FILE REFERENCE: CHL-T107C322

; CURRENT APPLICATION NUMBER: US/11/190,122  
; CURRENT FILING DATE: 2005-07-25  
; PRIOR APPLICATION NUMBER: 60/344,704  
; PRIOR FILING DATE: 2001-12-26  
; PRIOR APPLICATION NUMBER: 10/500,351  
; PRIOR FILING DATE: 2004-06-25  
; PRIOR APPLICATION NUMBER: pct/us2003/021157  
; PRIOR FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: 60/590,848  
; PRIOR FILING DATE: 2004-07-23  
; PRIOR APPLICATION NUMBER: 60/590,751  
; PRIOR FILING DATE: 2004-07-23  
; PRIOR APPLICATION NUMBER: 10/519,821  
; PRIOR FILING DATE: 2004-12-30  
; PRIOR APPLICATION NUMBER: 60/400,816  
; PRIOR FILING DATE: 2002-08-02  
; PRIOR APPLICATION NUMBER: 60/393,651  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: 60/393,428  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: PCT/US2002/041503  
; PRIOR FILING DATE: 2002-12-26  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 2800  
; TYPE: DNA  
; ORGANISM: ARTIFICIAL  
; FEATURE:  
; OTHER INFORMATION: aada/BADH expression cassette  
US-11-190-122-1

Query Match 77.3%; Score 102.8; DB 11; Length 2800;  
Best Local Similarity 90.3%; Pred. No. 3.2e-24;  
Matches 121; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGCTTCATAGAGATGATAGAGGCTGTGGATTGACGTGAGGGG 60  
Db 85 GCTCCCCCGCGCTTCATAGAGATGATAGAGGCTGTGGATTGACGTGAGGGG 144  
QY 61 CAGGATGCTATATTTCTGGAGCGAATCCGGCGAATGCAAGCGCTTGATACGT 119  
Db 145 CAGGATGCTATATTTCTGGAGCGAATCCGGCGAATGCAAGCGCTTGATACG 204  
QY 120 TGTAGGAGGAGATT 133  
Db 205 TGTAGGAGGAGATT 218

## RESULT 8

US-11-190-122-2  
; Sequence 2, Application US/11190122  
; Publication No. US20060031964A1  
; GENERAL INFORMATION:  
; APPLICANT: Daniell, Henry  
; TITLE OF INVENTION: Placid Genetic Engineering Via Somatic Embryogenesis  
; FILE REFERENCE: CHL-T107C322  
; CURRENT APPLICATION NUMBER: US/11/190,122  
; CURRENT FILING DATE: 2005-07-25  
; PRIOR APPLICATION NUMBER: 60/344,704  
; PRIOR FILING DATE: 2001-12-26  
; PRIOR APPLICATION NUMBER: 10/500,351  
; PRIOR FILING DATE: 2004-06-25  
; PRIOR APPLICATION NUMBER: pct/us2003/021157  
; PRIOR FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: 60/590,848  
; PRIOR FILING DATE: 2004-07-23  
; PRIOR APPLICATION NUMBER: 60/590,751  
; PRIOR FILING DATE: 2004-07-23  
; PRIOR APPLICATION NUMBER: 10/519,821  
; PRIOR FILING DATE: 2004-12-30  
; PRIOR APPLICATION NUMBER: 60/400,816  
; PRIOR FILING DATE: 2002-08-02

PRIOR APPLICATION NUMBER: 60/393,651  
PRIOR FILING DATE: 2002-07-03  
PRIOR APPLICATION NUMBER: 60/393,428  
PRIOR FILING DATE: 2002-07-03  
PRIOR APPLICATION NUMBER: PCT/US2002/041503  
PRIOR FILING DATE: 2002-12-26  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 2  
LENGTH: 3119  
TYPE: DNA  
ORGANISM: ARTIFICIAL  
FEATURE:  
OTHER INFORMATION: gfp/BADH expression cassette  
US-11-190-122-2

Query Match 77.3%; Score 102.8; DB 11; Length 3119;  
Best Local Similarity 90.3%; Pred. No. 3.2e-24;  
Matches 121; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCTTCATAGATGAGTGGATGCGTGGATGCGTGGAGGGG 60  
DB 79 GCTCCCCCGCTTCATAGATGAGTGGATGCGTGGATGCGTGGAGGGG 138  
QY 61 CAGGATGCTATA-TTCTGGAGCGAATCTCCGGCGAATACGAGCGCTTGATACAGT 119  
DB 139 CAGGATGCTATA-TTCTGGAGCGAATCTCCGGCGAATACGAGCGCTTGATACAG 198  
QY 120 TGTAGGAGGAGT 133  
DB 199 TTATGCTTGAAT 212

## RESULT 9

US-11-004-399-377  
Sequence 377, Application US/11004399  
Publication No. US20060053516A1  
GENERAL INFORMATION:  
APPLICANT: Chye, Mee Lee  
APPLICANT: Li, Hong Ye  
APPLICANT: Ramalingam, Sathiskumar  
APPLICANT: Poon, Leo Lit Man  
TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide  
TITLE OF INVENTION: Sequences and Methods of Use Thereof For Immunization Against SA  
FILE REFERENCE: 2587/73166/RDX  
CURRENT APPLICATION NUMBER: US/11/004,399  
CURRENT FILING DATE: 2004-12-03  
PRIOR APPLICATION NUMBER: US 60/527,637  
PRIOR FILING DATE: 2003-12-03  
NUMBER OF SEQ ID NOS: 4043  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 377  
LENGTH: 8040  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: pCV8  
US-11-004-399-377

Query Match 46.8%; Score 62.2; DB 11; Length 8040;  
Best Local Similarity 73.2%; Pred. No. 1.2e-10;  
Matches 93; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

QY 4 CCCCCCGCTTCATAGATGAGTGGATGCGTGGATGCGTGGAGGGGCG 63  
DB 3284 CCCCCCGCTTCATAGATGAGTGGATGCGTGGATGCGTGGAGGGGCG 3343  
QY 64 GGATGCTATA-TTCTGGAGCGAATCTCCGGCGAATACGAGCGCTTGATACAGTGT 122  
DB 3344 GGATGCTATA-TTCTGGAGCGAATCTCCGGCGAATACGAGCGCTTGATACAGTGT 3403  
QY 123 AGGAGG 129

DB 3404 AGGAGG 3410

## RESULT 10

US-11-004-399-378  
Sequence 378, Application US/11004399  
Publication No. US20060053516A1  
GENERAL INFORMATION:  
APPLICANT: Chye, Mee Lee  
APPLICANT: Li, Hong Ye  
APPLICANT: Ramalingam, Sathiskumar  
APPLICANT: Poon, Leo Lit Man  
TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide  
TITLE OF INVENTION: Sequences and Methods of Use Thereof For Immunization Against S  
FILE REFERENCE: 2587/73166/RDX  
CURRENT APPLICATION NUMBER: US/11/004,399  
CURRENT FILING DATE: 2004-12-03  
PRIOR APPLICATION NUMBER: US 60/527,637  
PRIOR FILING DATE: 2003-12-03  
NUMBER OF SEQ ID NOS: 4043  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 378  
LENGTH: 8082  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: pCV8  
NAME/KEY: CDS  
LOCATION: (1)..(8082)  
OTHER INFORMATION:  
US-11-004-399-378

Query Match 46.8%; Score 62.2; DB 11; Length 8082;  
Best Local Similarity 73.2%; Pred. No. 1.2e-10;  
Matches 93; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

QY 4 CCCCCCGCTTCATAGATGAGTGGATGCGTGGATGCGTGGAGGGGCG 63  
DB 3326 CCCCCCGCTTCATAGATGAGTGGATGCGTGGATGCGTGGAGGGGCG 3385  
QY 64 GGATGCTATA-TTCTGGAGCGAATCTCCGGCGAATACGAGCGCTTGATACAGTGT 122  
DB 3386 GGATGCTATA-TTCTGGAGCGAATCTCCGGCGAATACGAGCGCTTGATACAGTGT 3445  
QY 123 AGGAGG 129  
DB 3446 AGGAGG 3452

## RESULT 11

US-11-004-399-483  
Sequence 483, Application US/11004399  
Publication No. US20060053516A1  
GENERAL INFORMATION:  
APPLICANT: Chye, Mee Lee  
APPLICANT: Li, Hong Ye  
APPLICANT: Ramalingam, Sathiskumar  
APPLICANT: Poon, Leo Lit Man  
TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide  
TITLE OF INVENTION: Sequences and Methods of Use Thereof For Immunization Against S  
FILE REFERENCE: 2587/73166/RDX  
CURRENT APPLICATION NUMBER: US/11/004,399  
CURRENT FILING DATE: 2004-12-03  
PRIOR APPLICATION NUMBER: US 60/527,637  
PRIOR FILING DATE: 2003-12-03  
NUMBER OF SEQ ID NOS: 4043  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 483  
LENGTH: 8082

TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: pcv8  
NAME/KEY: CDS  
LOCATION: (2)..(8080)  
OTHER INFORMATION:  
US-11-004-399-483

Query Match 46.8%; Score 62.2; DB 11; Length 8082;  
Best Local Similarity 73.2%; Pred. No. 1.2e-10;  
Matches 93; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

QY 4 CCCCCCGCTGTTCAATGAGATGATGATGAGGCTCGTGGATTGACGTGAGGGGCGAG 63  
DB 3326 CCCCCCGACATCGAAGCGAATGATGATGAGGCTCGTGGATTGACGTGAGGGGCGAG 3385  
QY 64 GGATGGCTATA-TTCTGGAGCGAAGCTCCGGCGAATACGAAGCGCTTGATACAGTTGT 122  
DB 3386 GGTTGGCTATACGTGCTGGTGGCGAATCCAGGCTAATATCTGAAGCGCTTGAAAGTTGT 3445  
QY 123 AGGAGG 129  
DB 3446 AGGAGG 3452

## RESULT 12

US-11-004-399-605  
Sequence 605, Application US/11004399  
Publication No. US20060053516A1  
GENERAL INFORMATION:  
APPLICANT: Chye, Mee Lee  
APPLICANT: Li, Hong Ye  
APPLICANT: Ramalingam, Sathiskumar  
APPLICANT: Poon, Leo Lit Man  
APPLICANT: Peiris, Joseph Sriyal Malik  
TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide  
FILE REFERENCE: 2587/73166/RDX  
CURRENT APPLICATION NUMBER: US/11/004,399  
CURRENT FILING DATE: 2004-12-03  
PRIOR APPLICATION NUMBER: US 60/527,637  
PRIOR FILING DATE: 2003-12-03  
NUMBER OF SEQ ID NOS: 4043  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 605  
LENGTH: 8082  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: pcv8  
NAME/KEY: CDS  
LOCATION: (3)..(8081)  
OTHER INFORMATION:  
US-11-004-399-605

Query Match 46.8%; Score 62.2; DB 11; Length 8082;  
Best Local Similarity 73.2%; Pred. No. 1.2e-10;  
Matches 93; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

QY 4 CCCCCCGCTGTTCAATGAGATGATGATGAGGCTCGTGGATTGACGTGAGGGGCGAG 63  
DB 3326 CCCCCCGACATCGAAGCGAATGATGATGAGGCTCGTGGATTGACGTGAGGGGCGAG 3385  
QY 64 GGATGGCTATA-TTCTGGAGCGAAGCTCCGGCGAATACGAAGCGCTTGATACAGTTGT 122  
DB 3386 GGTTGGCTATACGTGCTGGTGGCGAATCCAGGCTAATATCTGAAGCGCTTGAAAGTTGT 3445  
QY 123 AGGAGG 129  
DB 3446 AGGAGG 3452

RESULT 13  
US-11-004-399-1  
Sequence 1, Application US/11004399  
Publication No. US20060053516A1  
GENERAL INFORMATION:  
APPLICANT: Chye, Mee Lee  
APPLICANT: Li, Hong Ye  
APPLICANT: Ramalingam, Sathiskumar  
APPLICANT: Poon, Leo Lit Man  
APPLICANT: Peiris, Joseph Sriyal Malik  
TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide  
FILE REFERENCE: 2587/73166/RDX  
CURRENT APPLICATION NUMBER: US/11/004,399  
CURRENT FILING DATE: 2004-12-03  
PRIOR APPLICATION NUMBER: US 60/527,637  
PRIOR FILING DATE: 2003-12-03  
NUMBER OF SEQ ID NOS: 4043  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 9348  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: pcv1  
NAME/KEY: CDS  
LOCATION: (1)..(9348)  
OTHER INFORMATION:  
US-11-004-399-1

Query Match 46.8%; Score 62.2; DB 11; Length 9348;  
Best Local Similarity 73.2%; Pred. No. 1.2e-10;  
Matches 93; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

QY 4 CCCCCCGCTGTTCAATGAGATGATGATGAGGCTCGTGGATTGACGTGAGGGGCGAG 63  
DB 4592 CCCCCCGACATCGAAGCGAATGATGATGAGGCTCGTGGATTGACGTGATGAGGGT 4651  
QY 64 GGATGGCTATA-TTCTGGAGCGAAGCTCCGGCGAATACGAAGCGCTTGATACAGTTGT 122  
DB 4652 GGTTGGCTATACGTGCTGGTGGCGAATCCAGGCTAATATCTGAAGCGCTTGAAAGTTGT 4711  
QY 123 AGGAGG 129  
DB 4712 AGGAGG 4718

## RESULT 14

US-11-004-399-113  
Sequence 113, Application US/11004399  
Publication No. US20060053516A1  
GENERAL INFORMATION:  
APPLICANT: Chye, Mee Lee  
APPLICANT: Li, Hong Ye  
APPLICANT: Ramalingam, Sathiskumar  
APPLICANT: Poon, Leo Lit Man  
APPLICANT: Peiris, Joseph Sriyal Malik  
TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide  
FILE REFERENCE: 2587/73166/RDX  
CURRENT APPLICATION NUMBER: US/11/004,399  
CURRENT FILING DATE: 2004-12-03  
PRIOR APPLICATION NUMBER: US 60/527,637  
PRIOR FILING DATE: 2003-12-03  
NUMBER OF SEQ ID NOS: 4043  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 113  
LENGTH: 9348  
TYPE: DNA  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: pcv1  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (2)..(9346)  
OTHER INFORMATION:  
US-11-004-399-113

Query Match 46.8%; Score 62.2; DB 11; Length 9348;  
Best Local Similarity 73.2%; Pred. No. 1.2e-10;  
Matches 93; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

QY 4 CCCCCCGCTGTTCAATGAGATGAAGAGCTGTGGATTGACGTGAGGGGACAG 63  
DB 4592 CCCCCCGCAAGATGAGACGGGAATGATAGAGCTTGTGGATTGACGTGATAGGGTAG 4651  
QY 64 GGATGCTATA-TTCTGGGAGCGAATCCGGGCGAATACGAAGCGCTTGATACAGTTGT 122  
DB 4652 GGTGGCTATACGTGCTGGGCGAAGCTCCAGCTTAATCTGAAGCGCTTGAGAGTTGT 4711  
QY 123 AGGGAGG 129  
DB 4712 AGGGAGG 4718

RESULT 15  
US-11-004-399-274  
Sequence 274, Application US/11004399  
Publication No. US20060053516A1  
GENERAL INFORMATION:  
APPLICANT: Chye, Mee Lee  
APPLICANT: Li, Hong Ye  
APPLICANT: Ramalingam, Sachiskumar  
APPLICANT: Poon, Leo Lit Man  
APPLICANT: Beiris, Joseph Sriyal Malik  
TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide  
FILE REFERENCE: 2587/73166/RDK  
CURRENT APPLICATION NUMBER: US/11/004,399  
CURRENT FILING DATE: 2004-12-03  
PRIOR APPLICATION NUMBER: US 60/527,637  
PRIOR FILING DATE: 2003-12-03  
NUMBER OF SEQ ID NOS: 4043  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 274  
LENGTH: 9348  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: pcv1  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (3)..(9347)  
OTHER INFORMATION:  
US-11-004-399-274

Query Match 46.8%; Score 62.2; DB 11; Length 9348;  
Best Local Similarity 73.2%; Pred. No. 1.2e-10;  
Matches 93; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

QY 4 CCCCCCGCTGTTCAATGAGATGAAGAGCTGTGGATTGACGTGAGGGGACAG 63  
DB 4592 CCCCCCGCAAGATGAGACGGGAATGATAGAGCTTGTGGATTGACGTGATAGGGTAG 4651  
QY 64 GGATGCTATA-TTCTGGGAGCGAATCCGGGCGAATACGAAGCGCTTGATACAGTTGT 122  
DB 4652 GGTGGCTATACGTGCTGGGCGAAGCTCCAGCTTAATCTGAAGCGCTTGAGAGTTGT 4711  
QY 123 AGGGAGG 129  
DB 4712 AGGGAGG 4718

Search completed: April 18, 2006, 00:03:30  
Job time : 365 secs

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: April 17, 2006, 23:49:25 ; Search time 454 Seconds  
(without alignments)  
2422.527 Million cell updates/sec

Title: US-10-663-241-32

Perfect score: 133  
Sequence: 1 gctcccccgcgcgtctcaaa.....tacagttgtaggaagagatt 133

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_NA\_Main: \*  
1: /cgn2\_6/ptodaca/1/pubpna/US07\_PUBCOMB.seq: \*  
2: /cgn2\_6/ptodaca/1/pubpna/US08\_PUBCOMB.seq: \*  
3: /cgn2\_6/ptodaca/1/pubpna/US09\_PUBCOMB.seq: \*  
4: /cgn2\_6/ptodaca/1/pubpna/US09A\_PUBCOMB.seq: \*  
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8: /cgn2\_6/ptodaca/1/pubpna/US10D\_PUBCOMB.seq: \*  
9: /cgn2\_6/ptodaca/1/pubpna/US10E\_PUBCOMB.seq: \*  
10: /cgn2\_6/ptodaca/1/pubpna/US11\_PUBCOMB.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	133	100.0	133	7	US-10-663-241-32
2	122	91.7	1143	6	US-10-460-716-2
3	122	91.7	1417	6	US-10-460-716-3
4	121	91.0	2145	7	US-10-473-207-26
5	119.4	89.8	1544	7	US-10-473-207-4
6	119.4	89.8	2391	7	US-10-473-207-25
7	107	80.5	119	8	US-10-881-813-6
8	102.8	77.3	220	7	US-10-095-514-3
9	102.8	77.3	233	8	US-10-737-251-38
10	102.8	77.3	6477	7	US-10-377-134-63
11	102.8	77.3	7652	7	US-10-680-824A-1
12	102.8	77.3	8684	7	US-10-680-824A-2
13	102.8	77.3	10011	7	US-10-680-824A-19
14	102.8	77.3	10011	9	US-10-957-562-4
15	96.2	72.3	8684	7	US-10-680-824A-2
16	94	70.7	183	6	US-10-358-253-16
17	93.2	70.1	233	6	US-10-737-251-41
18	91.6	68.9	234	8	US-10-737-251-41
19	87.4	65.7	202	3	US-09-843-324A-1
20	87.4	65.7	244	3	US-09-843-324A-2
21	83.6	63.0	112	8	US-10-737-251-3
22	83.6	62.9	237	8	US-10-737-251-43
23	83.6	62.9	1993	6	US-10-460-716-1

C	24	83.6	62.9	4586	6	US-10-460-716-4	Sequence 4, Appl
C	25	83.6	62.9	7455	5	US-10-219-227-19	Sequence 19, Appl
	26	82.2	61.8	112	8	US-10-737-251-22	Sequence 22, Appl
	27	80.8	60.8	112	8	US-10-737-251-4	Sequence 4, Appl
	28	80.6	60.6	112	8	US-10-737-251-21	Sequence 21, Appl
	29	80.6	60.6	112	8	US-10-737-251-23	Sequence 23, Appl
	30	79	59.4	112	8	US-10-737-251-6	Sequence 5, Appl
	31	79	59.4	112	8	US-10-737-251-1	Sequence 6, Appl
	32	79	59.4	112	8	US-10-737-251-7	Sequence 7, Appl
	33	79	59.4	112	8	US-10-737-251-8	Sequence 8, Appl
	34	79	59.4	112	8	US-10-737-251-9	Sequence 9, Appl
	35	79	59.4	112	8	US-10-737-251-10	Sequence 10, Appl
	36	79	59.4	112	8	US-10-737-251-11	Sequence 11, Appl
	37	79	59.4	112	8	US-10-737-251-12	Sequence 12, Appl
	38	79	59.4	112	8	US-10-737-251-13	Sequence 13, Appl
	39	79	59.4	112	8	US-10-737-251-14	Sequence 14, Appl
	40	79	59.4	112	8	US-10-737-251-15	Sequence 15, Appl
	41	79	59.4	112	8	US-10-737-251-16	Sequence 16, Appl
	42	79	59.4	112	8	US-10-737-251-17	Sequence 17, Appl
	43	79	59.4	112	8	US-10-737-251-18	Sequence 18, Appl
	44	79	59.4	112	8	US-10-737-251-19	Sequence 19, Appl
	45	79	59.4	112	8	US-10-737-251-20	Sequence 20, Appl

## ALIGNMENTS

RESULT 1  
US-10-663-241-32  
; Sequence 32, Application US/10663241  
; Publication No. US20040040058A1  
; GENERAL INFORMATION:  
; APPLICANT: Malliga, Pal  
; APPLICANT: Srilaxman, Priya  
; TITLE OF INVENTION: Plastid Promoters for Transgene  
; FILE REFERENCE: RUC 97-0097  
; CURRENT APPLICATION NUMBER: US/10/663,241  
; CURRENT FILING DATE: 2003-09-16  
; PRIOR APPLICATION NUMBER: US/09/445,283C  
; PRIOR FILING DATE: 1999-12-03  
; PRIOR APPLICATION NUMBER: PCT/US98/11437  
; PRIOR FILING DATE: 1998-06-03  
; PRIOR APPLICATION NUMBER: 60/058,670  
; PRIOR FILING DATE: 1997-09-12  
; PRIOR APPLICATION NUMBER: 60/048,376  
; PRIOR FILING DATE: 1997-06-03  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 133  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Prrn promoter  
US-10-663-241-32

Query Match 100.0%; Score 133; DB 7; Length 133;  
Best Local Similarity 100.0%; Pred. No. 1.3e-39;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GCTCCCCCGCGCTTCATGATGATGATAGAGCTCGTGGATTGACGAGGGGG	60
DB	1	GCTCCCCCGCGCTTCATGATGATGATAGAGCTCGTGGATTGACGAGGGGG	60
QY	61	CAGGATGCTATATTCTGGAGCGAATCTCGGCGCAATACGAAGCGTTGATACGTT	120
DB	61	CAGGATGCTATATTCTGGAGCGAATCTCGGCGCAATACGAAGCGTTGATACGTT	120
QY	121	GTAAGGAGGAGATT	133
DB	121	GTAAGGAGGAGATT	133

```

RESULT 2
US-10-460-716-2/c
; Sequence 2, Application US/10460716
; Publication No. US20030200568A1
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Skarjinskaja, Marina
; APPLICANT: Svab, Zora
; APPLICANT: Rutgers, The State University of New Jersey
; TITLE OF INVENTION: Plasmid Transformation in Legumella
; FILE REFERENCE: Rut 00-0109CIP
; CURRENT APPLICATION NUMBER: US/10/460,716
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US/09/524,087A
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: PCT/US97/03444
; PRIOR FILING DATE: 1997-03-06
; PRIOR APPLICATION NUMBER: 60/102,716
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Nicotianum tabacum
US-10-460-716-2

Query Match          91.7%; Score 122; DB 6; Length 1143;
Best Local Similarity 99.3%; Pred. No. 2.8e-35;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1  GGTCCCCCGCCGCTTCATAGATGATTAAGAGGCTCGTGGATTGACGTGAGGGG 60
DB      1130 GGTCCCCCGCCGCTTCATAGATGATTAAGAGGCTCGTGGATTGACGTGAGGGG 1071

QY      61  CAGGATGGCTATA-TTCTGGAGCGAACTCCGGCGGAATACGACGCTTGATCACT 119
DB      1070 CAGGATGGCTATAATTCTCGGAGCGAACTCCGGCGGAATACGACGCTTGATCACT 1011

QY      120 TGTAGGAGGAGATT 133
DB      1010 TGTAGGAGGAGATT 997

RESULT 3
US-10-460-716-3
; Sequence 3, Application US/10460716
; Publication No. US20030200568A1
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Skarjinskaja, Marina
; APPLICANT: Svab, Zora
; APPLICANT: Rutgers, The State University of New Jersey
; TITLE OF INVENTION: Plasmid Transformation in Legumella
; FILE REFERENCE: Rut 00-0109CIP
; CURRENT APPLICATION NUMBER: US/10/460,716
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US/09/524,087A
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: PCT/US97/03444
; PRIOR FILING DATE: 1997-03-06
; PRIOR APPLICATION NUMBER: 60/102,716
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1417
; TYPE: DNA
; ORGANISM: Artificial Sequence

```

```

; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-460-716-3

Query Match          91.7%; Score 122; DB 6; Length 1417;
Best Local Similarity 99.3%; Pred. No. 3e-35;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1  GGTCCCCCGCCGCTTCATAGATGATTAAGAGGCTCGTGGATTGACGTGAGGGG 60
DB      23  GGTCCCCCGCCGCTTCATAGATGATTAAGAGGCTCGTGGATTGACGTGAGGGG 82

QY      61  CAGGATGGCTATA-TTCTGGAGCGAACTCCGGCGGAATACGAAAGCGCTTGATCACT 119
DB      83  CAGGATGGCTATAATTCTCGGAGCGAACTCCGGCGGAATACGAAAGCGCTTGATCACT 142

QY      120 TGTAGGAGGAGATT 133
DB      143 TGTAGGAGGAGATT 156

RESULT 4
US-10-473-207-26
; Sequence 26, Application US/10473207
; Publication No. US20040163145A1
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Cornille, Sylvie
; APPLICANT: Lutz, Kerry
; TITLE OF INVENTION: Integrases for the insertion of
; FILE REFERENCE: 1594-RUT.01-091US
; CURRENT APPLICATION NUMBER: US/10/473,207
; PRIOR FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: PCT/US02/09537
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 60/279615
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 2145
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: plasmid fragment
US-10-473-207-26

Query Match          91.0%; Score 121; DB 7; Length 2145;
Best Local Similarity 99.2%; Pred. No. 7.7e-35;
Matches 132; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1  GGTCCCCCGCCGCTTCATAGATGATTAAGAGGCTCGTGGATTGACGTGAGGGG 60
DB      17  GGTCCCCCGCCGCTTCATAGATGATTAAGAGGCTCGTGGATTGACGTGAGGGG 76

QY      61  CAGGATGGCTATA-TTCTGGAGCGAACTCCGGCGGAATACGAAAGCGCTTGATCACT 119
DB      77  CAGGATGGCTATAATTCTCGGAGCGAACTCCGGCGGAATACGAAAGCGCTTGATCACT 136

QY      120 TGTAGGAGGAGATT 132
DB      137 TGTAGGAGGAGATT 149

RESULT 5
US-10-473-207-4/c
; Sequence 4, Application US/10473207
; Publication No. US20040163145A1
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Cornille, Sylvie
; APPLICANT: Lutz, Kerry

```

;; TITLE OF INVENTION: Integrases for the insertion of  
;; FILE OF INVENTION: heterologous nucleic acids into the plasmid genome  
;; FILE REFERENCE: 1594-RUT-01-091US  
;; CURRENT APPLICATION NUMBER: US/10/473,207  
;; CURRENT FILING DATE: 2003-09-19  
;; PRIOR APPLICATION NUMBER: PCT/US02/09537  
;; PRIOR FILING DATE: 2002-03-29  
;; PRIOR APPLICATION NUMBER: 60/279615  
;; PRIOR FILING DATE: 2001-03-29  
;; NUMBER OF SEQ ID NOS: 29  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 4  
;; LENGTH: 1544  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: vector insert  
US-10-473-207-4

Query Match 89.8%; Score 119.4; DB 7; Length 1544;  
Best Local Similarity 98.5%; Pred. No. 2.9e-34;  
Matches 131; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGCTGTTCAATGAGATGATTAAGAGGCTCTGTGGATTGACGTGAGGGG 60  
DB 1393 GCTCCCCCGCGCTGTTCAATGAGATGATTAAGAGGCTCTGTGGATTGACGTGAGGGG 1334  
QY 61 CAGGATGCGCTATA-TTCTGGAGCGAATCCGGGGCGAATACAGAGCGCTTGATACGT 119  
DB 1333 CAGGATGCGCTATA-TTCTGGAGCGAATCCGGGGCGAATACAGAGCGCTTGATACGT 1274  
QY 120 TGTAGGAGGGAT 132  
DB 1273 TGTAGGAGGGAT 1261

## RESULT 6

US-10-473-207-25  
;; Sequence 25, Application US/10473207  
;; Publication No. US20040163145A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Maliga, Pal  
;; APPLICANT: Cornille, Sylvie  
;; APPLICANT: Lutz, Kerry  
;; TITLE OF INVENTION: Integrases for the insertion of  
;; FILE REFERENCE: 1594-RUT-01-091US  
;; CURRENT APPLICATION NUMBER: US/10/473,207  
;; CURRENT FILING DATE: 2003-09-19  
;; PRIOR APPLICATION NUMBER: PCT/US02/09537  
;; PRIOR FILING DATE: 2002-03-29  
;; PRIOR APPLICATION NUMBER: 60/279615  
;; PRIOR FILING DATE: 2001-03-29  
;; NUMBER OF SEQ ID NOS: 29  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 25  
;; LENGTH: 2391  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: plasmid fragment  
US-10-473-207-25

Query Match 89.8%; Score 119.4; DB 7; Length 2391;  
Best Local Similarity 98.5%; Pred. No. 3.1e-34;  
Matches 131; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGCTGTTCAATGAGATGATTAAGAGGCTCTGTGGATTGACGTGAGGGG 60  
DB 13 GCTCCCCCGCGCTGTTCAATGAGATGATTAAGAGGCTCTGTGGATTGACGTGAGGGG 72  
QY 61 CAGGATGCGCTATA-TTCTGGAGCGAATCCGGGGCGAATACAGAGCGCTTGATACGT 119

DB 73 CAGGATGCGCTATA-TTCTGGAGCGAATCCGGGGCGAATACAGAGCGCTTGATACGT 132  
QY 120 TGTAGGAGGGAT 132  
DB 133 TGTAGGAGGGAT 145

## RESULT 7

US-10-881-813-6  
;; Sequence 6, Application US/10881813  
;; Publication No. US20050044593A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Cox, Kevin  
;; APPLICANT: Peele, Charles G.  
;; TITLE OF INVENTION: Chloroplast Transformation of Duckweed  
;; FILE REFERENCE: 40989/279944  
;; CURRENT APPLICATION NUMBER: US/10/881,813  
;; CURRENT FILING DATE: 2004-06-30  
;; PRIOR APPLICATION NUMBER: US 60/484,166  
;; PRIOR FILING DATE: 2003-07-01  
;; PRIOR APPLICATION NUMBER: US 60/492,179  
;; PRIOR FILING DATE: 2003-08-01  
;; NUMBER OF SEQ ID NOS: 12  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 6  
;; LENGTH: 119  
;; TYPE: DNA  
;; ORGANISM: Nicotiana tabacum  
US-10-881-813-6

Query Match 80.5%; Score 107; DB 8; Length 119;  
Best Local Similarity 99.2%; Pred. No. 7.7e-30;  
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGCTGTTCAATGAGATGATTAAGAGGCTCTGTGGATTGACGTGAGGGG 60  
DB 1 GCTCCCCCGCGCTGTTCAATGAGATGATTAAGAGGCTCTGTGGATTGACGTGAGGGG 60  
QY 61 CAGGATGCGCTATA-TTCTGGAGCGAATCCGGGGCGAATACAGAGCGCTTGATACGT 118  
DB 61 CAGGATGCGCTATA-TTCTGGAGCGAATCCGGGGCGAATACAGAGCGCTTGATACGT 119

## RESULT 8

US-10-095-514-3  
;; Sequence 3, Application US/10095514  
;; Publication No. US20040093658A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Sasaki, Yukiko  
;; APPLICANT: Yokota, Akiko  
;; APPLICANT: Madoka, Yuka  
;; TITLE OF INVENTION: Method for Promoting Fatty Acid Synthesis in a Plant  
;; FILE REFERENCE: 026350-072  
;; CURRENT APPLICATION NUMBER: US/10/095,514  
;; CURRENT FILING DATE: 2002-03-13  
;; PRIOR APPLICATION NUMBER: JP 2001-70,691  
;; PRIOR FILING DATE: 2001-03-13  
;; PRIOR APPLICATION NUMBER: JP 2001-300,038  
;; PRIOR FILING DATE: 2001-09-28  
;; NUMBER OF SEQ ID NOS: 11  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 3  
;; LENGTH: 220  
;; TYPE: DNA  
;; ORGANISM: N. tabacum cv. Xanthi  
US-10-095-514-3

Query Match 77.3%; Score 102.8; DB 7; Length 220;  
Best Local Similarity 90.3%; Pred. No. 3.3e-28;  
Matches 121; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGCTGTTCAATGAGATGATTAAGAGGCTCTGTGGATTGACGTGAGGGG 60

```
Db      30 GCTCCCCCGCGCTGTTCAATGAGATGAGATGAGAGCTGCTGGGATGACGTGAGGGG 89
Qy      61 CAGGATGGCTATA-TTCTGGAGGCGAAGCTCCGGCGGAATGAGAGCGCTTGATCACT 119
      |||
Db      90 CAGGATGGCTATATTCTTGGAGGCGAAGCTCCGGCGGAATGAGAGCGATGATCAAG 149
Qy      120 TGTAGGAGGATT 133
      |||
Db      150 TTATGCTTGAAT 163

RESULT 9
US-10-737-251-38
; Sequence 38, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Malliga
; APPLICANT: Jon Y. Suzuki
; TITLE OF INVENTION: Plasmid rRNA Operon Promoter/Elements for
; TITLE OF INVENTION: Construction of Chimeric Promoters for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; SOFTWARE: FastSeq for Windows Version 3.0
; NUMBER OF SEQ ID NOS: 51
; SEQ ID NO 38
; LENGTH: 233
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
US-10-737-251-38

Query Match      77.3%; Score 102.8; DB 8; Length 233;
Best Local Similarity 90.3%; Pred. No. 3.4e-28;
Matches 121; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy      1 GCTCCCCCGCGCTGTTCAATGAGATGAGATGAGAGCTGCTGGGATGACGTGAGGGG 60
Db      34 GCTCCCCCGCGCTGTTCAATGAGATGAGATGAGAGCTGCTGGGATGACGTGAGGGG 93
Qy      61 CAGGATGGCTATA-TTCTGGAGGCGAAGCTCCGGCGGAATGAGAGCGCTTGATCACT 119
      |||
Db      94 CAGGATGGCTATATTCTTGGAGGCGAAGCTCCGGCGGAATGAGAGCGATGATCAAG 153
Qy      120 TGTAGGAGGATT 133
      |||
Db      154 TTATGCTTGAAT 167

RESULT 10
US-10-377-134-63/c
; Sequence 63, Application US/10377134
; Publication No. US20040096938A1
; GENERAL INFORMATION:
; APPLICANT: XU, Ming-Qun
; APPLICANT: EVANS, Thomas C.
; APPLICANT: PRADHAN, Sriharsha
; APPLICANT: COMB, Donald G.
; APPLICANT: PAULUS, Henry
; APPLICANT: SUN, Luo
; APPLICANT: CHEN, Lixin
; APPLICANT: GHOSH, Inca
; TITLE OF INVENTION: METHOD FOR GENERATING SPLIT, NON-TRANSFERABLE GENES
; TITLE OF INVENTION: THAT ARE ABLE TO EXPRESS AN ACTIVE PROTEIN PRODUCT
; FILE REFERENCE: NEB-219
; CURRENT APPLICATION NUMBER: US/10/377,134
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: 09/936,588
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/US00/14122
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/135,677
```

```
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 6477
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Nucleotides 1-2482; E. coli vector pLITMUS28 (New
; OTHER INFORMATION: England Biolabs, Inc.)
; FEATURE:
; OTHER INFORMATION: Nucleotides 2493-6242; Nicotiana tabacum
; FEATURE:
; OTHER INFORMATION: Nucleotides 6243-6477; E. coli vector pLITMUS28
US-10-377-134-63

Query Match      77.3%; Score 102.8; DB 7; Length 6477;
Best Local Similarity 90.3%; Pred. No. 6.7e-28;
Matches 121; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy      1 GCTCCCCCGCGCTGTTCAATGAGATGAGATGAGAGCTGCTGGGATGACGTGAGGGG 60
Db      4014 GCTCCCCCGCGCTGTTCAATGAGATGAGATGAGAGCTGCTGGGATGACGTGAGGGG 3955
Qy      61 CAGGATGGCTATA-TTCTGGAGGCGAAGCTCCGGCGGAATGAGAGCGCTTGATCACT 119
      |||
Db      3954 CAGGATGGCTATATTCTTGGAGGCGAAGCTCCGGCGGAATGAGAGCGATGATCAAG 3895
Qy      120 TGTAGGAGGATT 133
      |||
Db      3894 TTATGCTTGAAT 3881

RESULT 11
US-10-680-824A-1/c
; Sequence 1, Application US/10680824A
; Publication No. US20040133937A1
; GENERAL INFORMATION:
; APPLICANT: Boudreau, Eric
; APPLICANT: Gu, Weining
; APPLICANT: De Fremond, Anic
; APPLICANT: Helfetz, Peter
; TITLE OF INVENTION: Plasmid Transformation
; FILE REFERENCE: 70149USNP
; CURRENT APPLICATION NUMBER: US/10/680,824A
; PRIOR FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/418596
; SOFTWARE: PatentIn version 3.1
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 1
; LENGTH: 7652
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pEBPoc plasmid transformation vector (Example 1 VII).
US-10-680-824A-1

Query Match      77.3%; Score 102.8; DB 7; Length 7652;
Best Local Similarity 90.3%; Pred. No. 6.9e-28;
Matches 121; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy      1 GCTCCCCCGCGCTGTTCAATGAGATGAGATGAGAGCTGCTGGGATGACGTGAGGGG 60
Db      6644 GCTCCCCCGCGCTGTTCAATGAGATGAGATGAGAGCTGCTGGGATGACGTGAGGGG 6585
Qy      61 CAGGATGGCTATA-TTCTGGAGGCGAAGCTCCGGCGGAATGAGAGCGCTTGATCACT 119
      |||
Db      6584 CAGGATGGCTATATTCTTGGAGGCGAAGCTCCGGCGGAATGAGAGCGATGATCAAG 6525
Qy      120 TGTAGGAGGATT 133
      |||
```

Db 6524 TTATGCTTGGAA 6511

## RESULT 12

US-10-680-824A-2

```
; Sequence 2, Application US/10680824A
; Publication No. US20040133937A1
; GENERAL INFORMATION:
; APPLICANT: Boudreau, Eric
; APPLICANT: Gu, Weining
; APPLICANT: De Framond, Anic
; APPLICANT: Helfetz, Peter
; TITLE OF INVENTION: Plasmid Transformation
; FILE REFERENCE: 70149USNP
; CURRENT APPLICATION NUMBER: US/10/680,824A
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/418596
; PRIOR FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 8684
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pEB8 (= pEB8a) plasmid transformation vector (Example 2).
```

## Query Match

77.3%; Score 102.8; DB 7; Length 8684;  
Best Local Similarity 90.3%; Pred. No. 7.1e-28;  
Matches 121; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

```
QY 1 GCTCCCCCGCGTCTCAATGAGATGATTAAGAGCTCGTGGATTGACGTGAGGGGG 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 2492 GCTCCCCCGCGTCTCAATGAGATGATTAAGAGCTCGTGGATTGACGTGAGGGGG 2551
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 CAGGGATGCTATA-TTCTGGAGCGAATCTCCGGCGAATACGAAGCGTTGATACAGT 119
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 2552 CAGGGATGCTATA-TTCTGGAGCGAATCTCCGGCGAATACGAAGCGTTGATACAG 2611
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 120 TGTAGGAGGAGT 133
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 2612 TTATGCTTGGAA 2625
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

## RESULT 13

US-10-680-824A-19

```
; Sequence 19, Application US/10680824A
; Publication No. US20040133937A1
; GENERAL INFORMATION:
; APPLICANT: Boudreau, Eric
; APPLICANT: Gu, Weining
; APPLICANT: De Framond, Anic
; APPLICANT: Helfetz, Peter
; TITLE OF INVENTION: Plasmid Transformation
; FILE REFERENCE: 70149USNP
; CURRENT APPLICATION NUMBER: US/10/680,824A
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/418596
; PRIOR FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 10011
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pEB10
```

US-10-680-824A-19

Query Match 77.3%; Score 102.8; DB 7; Length 10011;  
Best Local Similarity 90.3%; Pred. No. 7.3e-28;  
Matches 121; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGTCTCAATGAGATGATTAAGAGCTCGTGGATTGACGTGAGGGGG 60

DB 4372 GCTCCCCCGCGTCTCAATGAGATGATTAAGAGCTCGTGGATTGACGTGAGGGGG 4431

QY 61 CAGGGATGCTATA-TTCTGGAGCGAATCTCCGGCGAATACGAAGCGTTGATACAGT 119

DB 4432 CAGGGATGCTATA-TTCTGGAGCGAATCTCCGGCGAATACGAAGCGTTGATACAG 4491

QY 120 TGTAGGAGGAGT 133

DB 4492 TTATGCTTGGAA 4505

## RESULT 14

US-10-957-562-4

```
; Sequence 4, Application US/10957562
; Publication No. US2005007641A1
; GENERAL INFORMATION:
; APPLICANT: Syngenta Participations AG
; APPLICANT: Boudreau, Eric
; TITLE OF INVENTION: Promoter Functional in Plant Plasmids
; FILE REFERENCE: 70318WOPT
; CURRENT APPLICATION NUMBER: US/10/957,562
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/509,002
; PRIOR FILING DATE: 2003-10-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 10011
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid
; NAME/KEY: misc feature
; LOCATION: (1)..(10011)
```

US-10-957-562-4

Query Match 77.3%; Score 102.8; DB 9; Length 10011;  
Best Local Similarity 90.3%; Pred. No. 7.3e-28;  
Matches 121; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGTCTCAATGAGATGATTAAGAGCTCGTGGATTGACGTGAGGGGG 60

DB 4372 GCTCCCCCGCGTCTCAATGAGATGATTAAGAGCTCGTGGATTGACGTGAGGGGG 4431

QY 61 CAGGGATGCTATA-TTCTGGAGCGAATCTCCGGCGAATACGAAGCGTTGATACAGT 119

DB 4432 CAGGGATGCTATA-TTCTGGAGCGAATCTCCGGCGAATACGAAGCGTTGATACAG 4491

QY 120 TGTAGGAGGAGT 133

DB 4492 TTATGCTTGGAA 4505

## RESULT 15

US-10-680-824A-2/c

```
; Sequence 2, Application US/10680824A
; Publication No. US20040133937A1
; GENERAL INFORMATION:
; APPLICANT: Boudreau, Eric
; APPLICANT: Gu, Weining
; APPLICANT: De Framond, Anic
; APPLICANT: Helfetz, Peter
; TITLE OF INVENTION: Plasmid Transformation
; FILE REFERENCE: 70149USNP
; CURRENT APPLICATION NUMBER: US/10/680,824A
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/418596
; PRIOR FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 29
```

```
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2
/ LENGTH: 8684
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: pEB8 (= pEB8a) plasmid transformation vector (Example 2).
US-10-680-824A-2
```

```
Query Match          72.3%; Score 96.2; DB 7; Length 8684;
Best Local Similarity 95.3%; Pred. No. 2.1e-25;
Matches 121; Conservative 0; Mismatches 3; Indels 3; Gaps 2;
```

```
QY      8 CGCCGCTGTTCAATGAGATGATAAGAGGCTCGTGGAATTGACGTGAGGGGCAAGGAT 67
          |||||
DB      506 CGCCGCTGTTCAATGAGATGATAAGAGGCTCGTGGAATTGACGTGAGGGGCAAGGAT 447
QY      68 GGCCTATA-TTCTGGAGACCACTCCGGGCGAATACGAAGCGCTTGGATACAGTTGTAGG 126
          |||||
DB      446 GGCCTATATTCTGGAGACCACTCCGGGCGAATCTGAAGCGCTTGAT--AGTTGTAGG 389
QY      127 AGGGATT 133
          |||||
DB      388 AGGGATT 382
```

Search completed: April 17, 2006, 23:57:07  
Job time : 455 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceeleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 17, 2006, 23:46:06 ; Search time 148 Seconds  
(without alignments)  
1597.403 Million cell updates/sec

Title: US-10-663-241-32

Perfect score: 133  
Sequence: 1 gctcccccgcgtctcaaa.....tacagtttagtgaggggatt 133

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents NA.\*  
1: /cgn2\_6/ptodaca/1/ina/1.COMB.seq:\*  
2: /cgn2\_6/ptodaca/1/ina/5.COMB.seq:\*  
3: /cgn2\_6/ptodaca/1/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodaca/1/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodaca/1/ina/H.COMB.seq:\*  
6: /cgn2\_6/ptodaca/1/ina/PCTUS.COMB.seq:\*  
7: /cgn2\_6/ptodaca/1/ina/PP.COMB.seq:\*  
8: /cgn2\_6/ptodaca/1/ina/RB.COMB.seq:\*  
9: /cgn2\_6/ptodaca/1/ina/backfillseq.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	133	100.0	133	3	US-09-445-283C-32
2	122	91.7	165	3	US-08-189-256A-4
3	122	91.7	165	3	US-09-193-853-4
4	122	91.7	168	2	US-08-189-256A-2
5	122	91.7	168	3	US-09-193-853-2
6	122	91.7	1134	2	US-08-189-256A-10
7	122	91.7	1134	3	US-09-193-853-10
8	122	91.7	1143	3	US-09-142-114B-6
9	122	91.7	1416	2	US-08-189-256A-27
10	122	91.7	1416	3	US-09-193-853-27
11	122	91.7	1417	3	US-09-142-114B-7
12	122	91.7	161	2	US-08-189-256A-18
13	121	91.0	161	3	US-09-193-853-18
14	121	91.0	300	3	US-09-202-316-4
15	121	91.0	300	3	US-09-202-316-7
16	121	91.0	1208	2	US-08-189-256A-28
17	121	91.0	1208	3	US-09-193-853-28
18	118.8	89.3	150	2	US-08-189-256A-1
19	118.8	89.3	150	3	US-09-193-853-1
20	102.8	77.3	184	3	US-09-283-419-3
21	102.8	77.3	201	3	US-09-011-316-58
22	102.8	77.3	2962	2	US-08-189-256A-3
23	102.8	77.3	2962	3	US-09-193-853-3
24	102.8	77.3	6477	3	US-09-936-588-63

25	99.8	75.0	127	3	US-09-635-132-16	Sequence 16, Appl
26	88.8	66.8	164	2	US-08-189-256A-26	Sequence 26, Appl
27	88.8	66.8	164	3	US-09-193-853-26	Sequence 26, Appl
28	88.4	66.5	129	2	US-08-189-256A-25	Sequence 25, Appl
29	88.4	66.5	129	3	US-09-193-853-25	Sequence 25, Appl
30	88.4	66.5	140	2	US-08-189-256A-19	Sequence 19, Appl
31	88.4	66.5	140	3	US-09-193-853-19	Sequence 19, Appl
32	88	66.2	168	3	US-09-351-123-5	Sequence 5, Appl
33	88	66.2	258	2	US-08-189-256A-24	Sequence 24, Appl
34	88	66.2	258	3	US-09-193-853-24	Sequence 24, Appl
35	87.4	65.7	202	3	US-09-843-324A-1	Sequence 1, Appl
36	87.4	65.7	244	3	US-09-351-123-6	Sequence 6, Appl
37	87.4	65.7	244	3	US-09-843-324A-2	Sequence 2, Appl
38	83.6	62.9	369	3	US-09-265-919-10	Sequence 10, Appl
39	83.6	62.9	1993	3	US-09-142-114B-5	Sequence 5, Appl
40	83.6	62.9	7455	3	US-09-220-557-19	Sequence 19, Appl
41	83.6	62.9	7455	3	US-10-219-227-19	Sequence 19, Appl
42	82.6	62.1	117	2	US-08-217-360-14	Sequence 14, Appl
43	79.8	60.0	139	2	US-08-217-360-13	Sequence 13, Appl
44	77.2	58.0	146	2	US-08-217-360-17	Sequence 17, Appl
45	77.2	58.0	171	2	US-08-217-360-16	Sequence 16, Appl

## ALIGNMENTS

RESULT 1  
US-09-445-283C-32  
Sequence 32, Application US/09445283C  
Patent No. 6624296  
GENERAL INFORMATION:  
APPLICANT: Malliga, Pal  
APPLICANT: Silhavy, Daniel  
APPLICANT: Striman, Priya  
TITLE OR INVENTION: Placid Promoters for Transgene  
FILE REFERENCE: RUC 97-0097  
CURRENT APPLICATION NUMBER: US/09-445,283C  
PRIOR FILING DATE: 1999-12-03  
PRIOR APPLICATION NUMBER: PCT/US98/11437  
PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/058,670  
PRIOR FILING DATE: 1997-09-12  
PRIOR APPLICATION NUMBER: 60/048,376  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 32  
LENGTH: 133  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Pryn promoter  
US-09-445-283C-32

Query Match 100.0%; Score 133; DB 3; Length 133;  
Best Local Similarity 100.0%; Pred. No. 4.5e-39;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCCCCCGCGTTCATGAGTAAGAGAGGCTGTGAGTTGACGTGAGGGG 60  
1 GCTCCCCCGCGTTCATGAGTAAGAGAGGCTGTGAGTTGACGTGAGGGG 60  
DB 61 CAGGATGCTATATTTCTGGAGCCGAATCCGGCCGAATTCGAAGCGCTTGATCAGTT 120  
61 CAGGATGCTATATTTCTGGAGCCGAATCCGGCCGAATTCGAAGCGCTTGATCAGTT 120  
QY 121 GTAGGAGGAGATT 133  
121 GTAGGAGGAGATT 133  
DB 121 GTAGGAGGAGATT 133

RESULT 2

```

US-08-189-256A-4
: Sequence 4, Application US/08189256A
: Patent No. 5877402
: GENERAL INFORMATION:
:   APPLICANT: Maliga, Pal
:   APPLICANT: Svab, Zora
:   APPLICANT: Staub, Jeffrey
:   APPLICANT: Zoubenko, Oleg V.
:   APPLICANT: Allison, Lori A.
:   APPLICANT: Carrier, Helaine
:   APPLICANT: Kanevski, Ivan
:   TITLE OF INVENTION: DNA Constructs and Methods for Stably
:   TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
:   NUMBER OF SEQUENCES: 47
: CORRESPONDENCE ADDRESS:
:   ADDRESSEE: Dann, Dorfman, Herrell and Skillman
:   STREET: 1601 Market Street Suite 720
:   CITY: Philadelphia
:   STATE: PA
:   COUNTRY: USA
:   ZIP: 19103-2307
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: PatentIn Release #1.0, Version #1.30
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/08/189,256A
:     FILING DATE: 31-JAN-1994
:     CLASSIFICATION: 435
:     PRIOR APPLICATION NUMBER: US 08/111,398
:     APPLICATION NUMBER: US 08/111,398
:     FILING DATE: 25-AUG-1993
:     PRIOR APPLICATION DATA:
:       APPLICATION NUMBER: US 07/518,763
:       FILING DATE: 01-MAY-1990
:       ATTORNEY/AGENT INFORMATION:
:         NAME: Reed, Janet E.
:         REGISTRATION NUMBER: 36,252
:         TELECOMMUNICATION INFORMATION:
:           TELEPHONE: (215) 563-4100
:           TELEFAX: (215) 563-4044
:       INFORMATION FOR SEQ ID NO: 4:
:         SEQUENCE CHARACTERISTICS:
:           LENGTH: 165 base pairs
:           TYPE: nucleic acid
:           STRANDEDNESS: single
:           TOPOLOGY: linear
:         MOLECULE TYPE: DNA (genomic)
:         HYPOTHEetical: NO
:         ANTI-SENSE: NO
: US-08-189-256A-4
:
: Query Match          91.7%;   Score 122;   DB 2;   Length 165;
: Best Local Similarity 99.3%;   Pred. No. 5.2e-35;
: Matches 133;   Conservative 0;   Mismatches 0;   Indels 1;   Gaps 14
:
: QY      1  GCTCCCCCGCGTGGTCAATGAGAAATGAGATGAGAGGCTCGTGGGATTGACGTGAGGGGG 60
: Db      1  GCTCCCCCGCGTGGTCAATGAGAAATGAGATGAGAGGCTCGTGGGATTGACGTGAGGGGG 60
:
: QY      61  CAGGATGGCTATTA-TTCTGGAGAGCAATCCGGGCGAATACGAACGCTTGATACAGT 119
: Db      61  CAGGATGGCTATTAATTCTGGAGAGCAATCCGGGCGAATACGAACGCTTGATACAGT 120
:
: QY      120  TGTAGGAGGGATT 133
: Db      121  TGTAGGAGGGATT 134

```

RESULT 3  
US-09-193-853-4

Sequence 4 Application US/09192853  
Patent No. 6388168  
GENERAL INFORMATION:  
APPLICANT: Maliga, Pal  
APPLICANT: Svab, Zora  
APPLICANT: Staub, Jeffrey  
APPLICANT: Zoubenko, Oleg V.  
APPLICANT: Allison, Lori A.  
APPLICANT: Carver, Helaine  
APPLICANT: Kanevski, Ivan  
TITLE OF INVENTION: DNA Constructs and Methods for Stably  
TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and  
TITLE OF INVENTION: Expressing Recombinant Proteins Therein  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dann, Dorfman, Herrell and Skillman  
STREET: 1601 Market Street Suite 720  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103-2307  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/193,853  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/189,256  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/518,763  
FILING DATE: 01-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Reed, Janet E.  
REGISTRATION NUMBER: 36,252  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 563-4100  
TELEFAX: (215) 563-4044  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 165 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-193-853-4

RESULT 4  
US-08-189-256A-2  
; Sequence 2, Application US/08189256A

Patent No. 5877402  
GENERAL INFORMATION:  
APPLICANT: Maliga, Pal  
APPLICANT: Svab, Zora  
APPLICANT: Staud, Jeffrey  
APPLICANT: Zoubenko, Oleg V.  
APPLICANT: Allison, Lori A.  
APPLICANT: Carreer, Helaine  
APPLICANT: Kanevsk, Ivan  
TITLE OF INVENTION: DNA Constructs and Methods for Stably  
TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Damm, Dorfman, Herrell and Skillman  
STREET: 1601 Market Street Suite 720  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103-2307  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/189,256A  
FILING DATE: 31-JAN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/111,398  
FILING DATE: 25-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/518,763  
FILING DATE: 01-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Reed, Janet E.  
REGISTRATION NUMBER: 36,252  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 563-4100  
TELEFAX: (215) 563-4044  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 168 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-189-256A-2

Query Match 91.7%; Score 122; DB 2; Length 168;  
Best Local Similarity 99.3%; Pred. No. 5.2e-35;  
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 GCTCCCCCGCGCTGTTCAATGAGATGATAGAGGCTGTGGGATTGACGAGGGGG 60  
DB 1 GCTCCCCCGCGCTGTTCAATGAGATGATAGAGGCTGTGGGATTGACGAGGGGG 60  
QY 61 CAGGAGTGGCTATA-TTCTGGAGCGAATCTCCGGCGGAATACGAAGCGCTTGATACAGT 119  
DB 61 CAGGAGTGGCTATA-TTCTGGAGCGAATCTCCGGCGGAATACGAAGCGCTTGATACAGT 120  
QY 120 TGTAGGAGGGATT 133  
DB 121 TGTAGGAGGGATT 134

RESULT 5  
US-09-193-853-2  
Sequence 2, Application US/09193853  
Patent No. 6386168

GENERAL INFORMATION:  
APPLICANT: Maliga, Pal  
APPLICANT: Svab, Zora  
APPLICANT: Staud, Jeffrey  
APPLICANT: Zoubenko, Oleg V.  
APPLICANT: Allison, Lori A.  
APPLICANT: Carreer, Helaine  
APPLICANT: Kanevsk, Ivan  
TITLE OF INVENTION: DNA Constructs and Methods for Stably  
TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Damm, Dorfman, Herrell and Skillman  
STREET: 1601 Market Street Suite 720  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103-2307  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/193,853  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/189,256  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/518,763  
FILING DATE: 01-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Reed, Janet E.  
REGISTRATION NUMBER: 36,252  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 563-4100  
TELEFAX: (215) 563-4044  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 168 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-193-853-2

Query Match 91.7%; Score 122; DB 3; Length 168;  
Best Local Similarity 99.3%; Pred. No. 5.2e-35;  
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 GCTCCCCCGCGCTGTTCAATGAGATGATAGAGGCTGTGGGATTGACGAGGGGG 60  
DB 1 GCTCCCCCGCGCTGTTCAATGAGATGATAGAGGCTGTGGGATTGACGAGGGGG 60  
QY 61 CAGGAGTGGCTATA-TTCTGGAGCGAATCTCCGGCGGAATACGAAGCGCTTGATACAGT 119  
DB 61 CAGGAGTGGCTATA-TTCTGGAGCGAATCTCCGGCGGAATACGAAGCGCTTGATACAGT 120  
QY 120 TGTAGGAGGGATT 133  
DB 121 TGTAGGAGGGATT 134

RESULT 6  
US-08-189-256A-10/C  
Sequence 10, Application US/08189256A  
Patent No. 5877402  
GENERAL INFORMATION:

```

; APPLICANT: Maliga, Pal
; APPLICANT: Svab, Zora
; APPLICANT: Straub, Jeffrey
; APPLICANT: Zoubenko, Oleg V.
; APPLICANT: Allison, Lori A.
; APPLICANT: Carter, Helaine
; APPLICANT: Kanevski, Ivan
; TITLE OF INVENTION: DNA Constructs and Methods for Stably
; TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/189,256A
; FILING DATE: 31-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/111,398
; FILING DATE: 25-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/518,763
; FILING DATE: 01-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1134 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-189-256A-10

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Query Match          91.7%; Score 122; DB 2; Length 1134;
Best Local Similarity 99.3%; Pred. No. 1e-34;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 GCTCCCCCGCGTCTTCAATGAGATGAAGAGGCTCTGAGATTGACGTGAGGGG 60
DB 1058 GCTCCCCCGCGTCTTCAATGAGATGAAGAGGCTCTGAGATTGACGTGAGGGG 999
QY 61 CAGGATGGCTATA-TTCTGGAGGAGCACTCCGGGCGAATACGAAGCGCTTGATACAGT 119
DB 998 CAGGATGGCTATAATTCTGGAGGAGCACTCCGGGCGAATACGAAGCGCTTGATACAGT 939
QY 120 TGTAGGAGGAGATT 133
DB 938 TGTAGGAGGAGATT 925

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```

RESULT 7
US-09-193-853-10/c
; Sequence 10, Application US/09193853
; Patent No. 6386168
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal

```

```

; APPLICANT: Svab, Zora
; APPLICANT: Straub, Jeffrey
; APPLICANT: Zoubenko, Oleg V.
; APPLICANT: Allison, Lori A.
; APPLICANT: Carter, Helaine
; APPLICANT: Kanevski, Ivan
; TITLE OF INVENTION: DNA Constructs and Methods for Stably
; TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/193,853
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/189,256
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/518,763
; FILING DATE: 01-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1134 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-09-193-853-10

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Query Match          91.7%; Score 122; DB 3; Length 1134;
Best Local Similarity 99.3%; Pred. No. 1e-34;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 GCTCCCCCGCGTCTTCAATGAGATGAAGAGGCTCTGAGATTGACGTGAGGGG 60
DB 1058 GCTCCCCCGCGTCTTCAATGAGATGAAGAGGCTCTGAGATTGACGTGAGGGG 999
QY 61 CAGGATGGCTATA-TTCTGGAGGAGCACTCCGGGCGAATACGAAGCGCTTGATACAGT 119
DB 998 CAGGATGGCTATAATTCTGGAGGAGCACTCCGGGCGAATACGAAGCGCTTGATACAGT 939
QY 120 TGTAGGAGGAGATT 133
DB 938 TGTAGGAGGAGATT 925

```

```

RESULT 8
US-09-142-114B-6/c
; Sequence 6, Application US/09142114B
; Patent No. 6376744
; GENERAL INFORMATION:
; APPLICANT: Rutgers University
; APPLICANT: Maliga, Pal

```

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/111,398  
FILING DATE: 25-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/518,763  
FILING DATE: 01-MAY-1990  
ATTORNEY/AGENT INFORMATION:

CLASSIFICATION: PRIOR APPLICATION DATA.  
APPLICATION NUMBER: 08/189,256  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/518,763  
FILING DATE: 01-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Reed, Janet E.

REGISTRATION NUMBER: 36,252  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 563-4100  
TELEFAX: (215) 563-4044  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1416 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-193-853-27

Query Match 91.7%; Score 122; DB 3; Length 1416;  
Best Local Similarity 99.3%; Pred. No. 1.1e-34;  
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGCTGTTCAATGAGATGAGGCTCGTGGATTGACGTGAGGGG 60  
DB 22 GCTCCCCCGCGCTGTTCAATGAGATGAGGCTCGTGGATTGACGTGAGGGG 81  
QY 61 CAGGGATGGCTATA-TTCTGGAGCGCAACTCCGGCGGAATGCAAGCGCTTGATCACT 119  
DB 82 CAGGGATGGCTATAATTCTGGAGCGCAACTCCGGCGGAATGCAAGCGCTTGATCACT 141  
QY 120 TGTAGGAGGGGATT 133  
DB 142 TGTAGGAGGGGATT 155

## RESULT 11

US-09-142-114B-7  
Sequence 7, Application US/09142114B  
Patent No. 6376744  
GENERAL INFORMATION:  
APPLICANT: Rutgers University  
APPLICANT: Maliga, Pal  
APPLICANT: Sikdar, Samir R.  
APPLICANT: Reddy, Siva Vanga  
TITLE OF INVENTION: Plasmid Transformation in Arabidopsis  
FILE REFERENCE: 09/142,114  
CURRENT APPLICATION NUMBER: US/09/142,114B  
CURRENT FILING DATE: 1999-02-05  
PRIOR APPLICATION NUMBER: PCT/US97/03444  
PRIOR FILING DATE: 1997-03-06  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 7  
LENGTH: 1417  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Sequence source:/note="synthetic construct"  
Patent No. 6376744  
US-09-142-114B-7

Query Match 91.7%; Score 122; DB 3; Length 1417;  
Best Local Similarity 99.3%; Pred. No. 1.1e-34;  
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGCTGTTCAATGAGATGAGGCTCGTGGATTGACGTGAGGGG 60  
DB 23 GCTCCCCCGCGCTGTTCAATGAGATGAGGCTCGTGGATTGACGTGAGGGG 82  
QY 61 CAGGGATGGCTATA-TTCTGGAGCGCAACTCCGGCGGAATGCAAGCGCTTGATCACT 119  
DB 83 CAGGGATGGCTATAATTCTGGAGCGCAACTCCGGCGGAATGCAAGCGCTTGATCACT 142  
QY 120 TGTAGGAGGGGATT 133  
DB 142 TGTAGGAGGGGATT 155

DB 143 TGTAGGAGGGGATT 156

## RESULT 12

US-08-189-256A-18  
Sequence 18, Application US/08189256A  
Patent No. 5877402  
GENERAL INFORMATION:  
APPLICANT: Maliga, Pal  
APPLICANT: Svab, Zora  
APPLICANT: Staub, Jeffrey  
APPLICANT: Zoubenko, Oleg V.  
APPLICANT: Allison, Lori A.  
APPLICANT: Carrier, Helaine  
APPLICANT: Kanevski, Ivan  
TITLE OF INVENTION: DNA Constructs and Methods for Stably  
TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and  
TITLE OF INVENTION: Expressing Recombinant Proteins Therein  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dann, Dorfman, Herrell and Skillman  
STREET: 1601 Market Street Suite 720  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103-2307  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/189,256A  
FILING DATE: 31-JAN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/111,398  
FILING DATE: 25-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/518,763  
FILING DATE: 01-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Reed, Janet E.  
REGISTRATION NUMBER: 36,252  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 563-4100  
TELEFAX: (215) 563-4044  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 161 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-189-256A-18

Query Match 91.0%; Score 121; DB 2; Length 161;  
Best Local Similarity 99.2%; Pred. No. 1.2e-34;  
Matches 132; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGCTGTTCAATGAGATGAGGCTCGTGGATTGACGTGAGGGG 60  
DB 23 GCTCCCCCGCGCTGTTCAATGAGATGAGGCTCGTGGATTGACGTGAGGGG 82  
QY 61 CAGGGATGGCTATA-TTCTGGAGCGCAACTCCGGCGGAATGCAAGCGCTTGATCACT 119  
DB 83 CAGGGATGGCTATAATTCTGGAGCGCAACTCCGGCGGAATGCAAGCGCTTGATCACT 142  
QY 120 TGTAGGAGGGGATT 132  
DB 143 TGTAGGAGGGGATT 155

RESULT 13  
US-09-193-853-18  
Sequence 18, Application US/09193853  
Patent No. 6388168  
GENERAL INFORMATION:  
APPLICANT: Maliga, Pal  
APPLICANT: Svab, Zora  
APPLICANT: Staeb, Jeffrey  
APPLICANT: Zoubenko, Oleg V.  
APPLICANT: Allison, Lori A.  
APPLICANT: Carreir, Helaine  
APPLICANT: Kanevski, Ivan  
TITLE OF INVENTION: DNA Constructs and Methods for Stably  
TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and  
TITLE OF INVENTION: Expressing Recombinant Proteins Therein  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dann, Dorfman, Herrell and Skillman  
STREET: 1601 Market Street Suite 720  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103-2307  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/193,853  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/189,256  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/518,763  
FILING DATE: 01-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Reed, Janet E.  
REGISTRATION NUMBER: 36,252  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 563-4100  
TELEFAX: (215) 563-4044  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 161 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-193-853-18

Query Match 91.0%; Score 121; DB 3; Length 161;  
Best Local Similarity 99.2%; Pred. No. 1.2e-34;  
Matches 132; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGTTCATGAGATGATAGAGGCTCGTGGATTGACGTAGGGGG 60  
DB 23 GCTCCCCCGCGTTCATGAGATGATAGAGGCTCGTGGATTGACGTAGGGGG 82

QY 61 CAGGATGGCTATA-TTCTGGAGCGAATCCGGCGGAATACGAAGCGTTGATACAGT 119  
DB 83 CAGGATGGCTATA-TTCTGGAGCGAATCCGGCGGAATACGAAGCGTTGATACAGT 142

QY 120 TGTAGGAGGAGAT 132  
DB 143 TGTAGGAGGAGAT 155

RESULT 14  
US-09-202-316-4  
Sequence 4, Application US/09202316  
Patent No. 6297054  
GENERAL INFORMATION:  
APPLICANT: Pal Maliga  
APPLICANT: Helaine Carreir  
APPLICANT: Sumita Chaudhuri  
TITLE OF INVENTION: Editing-Based Selectable Plasmid Marker  
TITLE OF INVENTION: Genes  
FILE REFERENCE: Rut-96-06041  
CURRENT APPLICATION NUMBER: US/09/202,316  
CURRENT FILING DATE: 1999-06-01  
PRIOR APPLICATION NUMBER: PCT/US97/10318  
PRIOR FILING DATE: 1997-06-13  
PRIOR APPLICATION NUMBER: 60/019,741  
PRIOR FILING DATE: 1996-06-14  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 300  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
US-09-202-316-4

Query Match 91.0%; Score 121; DB 3; Length 300;  
Best Local Similarity 99.2%; Pred. No. 1.5e-34;  
Matches 132; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGTTCATGAGATGATAGAGGCTCGTGGATTGACGTAGGGGG 60  
DB 17 GCTCCCCCGCGTTCATGAGATGATAGAGGCTCGTGGATTGACGTAGGGGG 76

QY 61 CAGGATGGCTATA-TTCTGGAGCGAATCCGGCGGAATACGAAGCGTTGATACAGT 119  
DB 77 CAGGATGGCTATA-TTCTGGAGCGAATCCGGCGGAATACGAAGCGTTGATACAGT 136

QY 120 TGTAGGAGGAGAT 132  
DB 137 TGTAGGAGGAGAT 149

RESULT 15  
US-09-202-316-7  
Sequence 7, Application US/09202316  
Patent No. 6297054  
GENERAL INFORMATION:  
APPLICANT: Pal Maliga  
APPLICANT: Helaine Carreir  
APPLICANT: Sumita Chaudhuri  
TITLE OF INVENTION: Editing-Based Selectable Plasmid Marker  
TITLE OF INVENTION: Genes  
FILE REFERENCE: Rut-96-06041  
CURRENT APPLICATION NUMBER: US/09/202,316  
CURRENT FILING DATE: 1999-06-01  
PRIOR APPLICATION NUMBER: PCT/US97/10318  
PRIOR FILING DATE: 1997-06-13  
PRIOR APPLICATION NUMBER: 60/019,741  
PRIOR FILING DATE: 1996-06-14  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 7  
LENGTH: 300  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
US-09-202-316-7

Query Match 91.0%; Score 121; DB 3; Length 300;

Best Local Similarity 99.2%; Pred. No. 1.5e-34;  
Matches 132; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy 1 GCTCCCCCGCGTTCATGAGATGATAGAGGCTCGTGGATTGACGTAGGGG 60
    |||||||
Db 17 GCTCCCCCGCGTTCATGAGATGATAGAGGCTCGTGGATTGACGTAGGGG 76
    |||||||
Qy 61 CAGGATGGCTATA-TTCTGGAGCGAGACTCCGGCGCAATACGAGCGCTTGATACAGT 119
    |||||||
Db 77 CAGGATGGCTATTTCTGGAGCGAGACTCCGGCGCAATACGAGCGCTTGATACAGT 136
    |||||||
Qy 120 TGTAGGAGAGGAT 132
    |||||||
Db 137 TGTAGGAGAGGAT 149
    |||||||
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Search completed: April 18, 2006, 00:25:54  
Job time : 149 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using bw model

Run on: April 17, 2006, 23:45:48 ; Search time 2980 Seconds  
(without alignments)  
2088.148 Million cell updates/sec

Title: US-10-663-241-32

Perfect score: 133  
Sequence: 1 gctcccccgcgcgtctcaaa.....tacagttcgtaggaaggatc 133

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 41078325 segs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_est3.\*  
4: gb\_est4.\*  
5: gb\_est5.\*  
6: gb\_est6.\*  
7: gb\_est7.\*  
8: gb\_est8.\*  
9: gb\_est9.\*  
10: gb\_est10.\*  
11: gb\_est11.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92.2	69.3	734	10	CG026772 PGAB74TR
2	91.6	68.9	415	7	CN930271 000322AFB
3	91.6	68.9	498	7	CN872595 020807AAP
4	91.6	68.9	510	1	AJ876197 AJ876197
5	91.6	68.9	598	7	CN871707 010128AAP
6	91.6	68.9	763	9	BH515735 BOKK79TR
7	91.6	68.9	764	10	CG026604 PGAB30TR
8	91.2	68.6	610	7	CK767400 PAM01-9ms
9	91.2	68.4	839	9	BH674012 BOMHD6TR
10	90.6	68.1	380	7	CN859023 000728AAA
11	85.4	64.2	491	9	BH009864 eg27602.x
12	85.2	64.1	770	9	BZ511771 BOMC72TR
13	85.2	64.1	773	9	BH424823 BOMN79TR
14	84.2	63.3	713	9	BH957918 odt85c05.
15	83.6	62.9	183	9	BZ483881 BOCAL29TR
16	83.6	62.9	199	9	BH537952 BOCGF8TR
17	83.6	62.9	238	9	BH677595 BOCMA9TR
18	83.6	62.9	292	9	BH474703 BOCG149TF
19	83.6	62.9	322	9	BH705426 BOMAG13TR
20	83.6	62.9	326	9	BZ440851 BOMN37TR
21	83.6	62.9	337	9	BZ464817 BOMN007TR
22	83.6	62.9	361	9	BZ470963 BOMBF24TR

23	83.6	62.9	367	9	BH430502
24	83.6	62.9	368	9	BH493122
25	83.6	62.9	407	9	BZ489878
26	83.6	62.9	416	9	BH664090
27	83.6	62.9	419	9	BH662193
28	83.6	62.9	422	9	BH475597
29	83.6	62.9	423	9	BH653681
30	83.6	62.9	434	9	BH545732
31	83.6	62.9	434	9	BH678091
32	83.6	62.9	435	9	BZ447238
33	83.6	62.9	441	9	BH657205
34	83.6	62.9	441	9	CC966698
35	83.6	62.9	448	9	BH689289
36	83.6	62.9	450	9	BH725279
37	83.6	62.9	451	9	BH719545
38	83.6	62.9	459	9	BH562132
39	83.6	62.9	466	9	BH541747
40	83.6	62.9	468	9	BH740372
41	83.6	62.9	469	9	BH718684
42	83.6	62.9	475	9	BH669610
43	83.6	62.9	475	9	BH700638
44	83.6	62.9	482	9	BH649351
45	83.6	62.9	484	9	BH650341

#### ALIGNMENTS

RESULT 1  
CG026772/c  
LOCUS  
DEFINITION PGAB74TR PGAB Carica papaya genomic clone PGAB74, genomic survey  
ACCESSION CG026772.1 GI:33898928  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Carica papaya (papaya)  
Carica papaya  
Bakariota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Caricaceae; Carica.  
1 (bases 1 to 734)  
Town, C.D., Van Aken, S., Utecherback, T., and Fraser, C.M.  
Whole genome shotgun sequencing of Carica papaya  
Unpublished (2003)  
Other\_GSSs: PGAB74TF  
Contact: Chris Town  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA.  
Tel: 301-838-3523  
Fax: 301-838-0208  
Email: cdtown@tigr.org  
DNA provided by Ray Ming was isolated from cultivar SunUp that was  
transgenic for papaya ringspot virus coat protein gene  
Seq primer: TR  
Class: sheared ends.  
Location/Qualifiers  
1..734  
/organism="Carica papaya"  
/mol\_type="genomic DNA"  
/cultivar="SunUp"  
/db\_xref="taxon:3649"  
/clone\_lib="PGAB74"  
/clone\_id="PGAB74"  
/note="Vector: pHS01, Site 1: BstXI, 2-3 kb sheared  
genomic DNA inserted into pHS01 using BstXI linkers"

#### ORIGIN

Query Match 69.3%; Score 92.2; DB 10; Length 734;  
Best Local Similarity 85.7%; Pred. No. 4.2e-19;  
Matches 114; Conservative 0; Mismatches 18; Indels 1; Gaps 1;  
QY 1 GCTCCCGCGCGTTCATGAGATGAGATGAGAGGCTGAGGATTGAGTGAAGGGG 60

Db	154	GCTCCCCCGCGTGTATGCAATAAGATTGAATAAGGGCTCGTGGAATTGACGTAGAAGGGG	
Oy	61	CAGGATATGCCTATA-TTCTGGAGCGAACTCCGGCGGAATACGAAGCCTTTGATACGT	119
Db	94	TAGGAGTAGCTATATTCTTCGGAGCGAAGCTCAGGCGGAATATGAAGCGCATGATACAAG	35
Oy	120	TGTAGGAGGGGAT	132
Db	34	TTATGCCCTTGAAT	22
RESULT 2			
LOCUS	CN872595	415 bp	mRNA linear EST 07-JUN-2004
DEFINITION	000322AFBC002396HT (AFBC) Royal Gala pre-opened floral bud Malus x domestica cDNA clone AFBC002396, mRNA sequence.		
ACCESSION	CN930271		
VERSION	CN930271.1	GI:48403084	
KEYWORDS	EST.		
SOURCE	Malus x domestica		
ORGANISM	Malus x domestica		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosoid; euroside I; Rosales; Rosaceae; Maloideae; Malus.		
AUTHORS	I (bases 1 to 415) Bennings,T., Bowen,U., Crowhurst,R., Gleave,A., Janssen,B., McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y.		
TITLE	HortResearch Apple EST Project		
JOURNAL	Unpublished (2004)		
COMMENT	Contact: Gleave, A. Sequencing Facility The Horticulture and Food Research Institute of New Zealand Ltd 120 Mt Albert Rd, Mt Albert, Auckland, New Zealand Tel: 00 64 09 815 4200 Fax: 00 64 09 815 4201 Email: est@hortresearch.co.nz.		
FEATURES			
source	Location/Qualifiers 1..415 /organism="Malus x domestica" /mol_type="mRNA" /db_xref="taxon:3750" /clone="AFBC002396" /tissue_type="Floral bud" /dev_stage="Pre-opening, flower at stage of nectar/pollen formation" /clone_id=""(AFBC) Royal Gala pre-opened floral bud" /note="Vector: pRK-CMV, library sequenced by Genesys Research & Development"		
ORIGIN			
Query Match	68.9%; Score 91.6; DB 7; Length 415;		
Best Local Similarity	85.1%; Pred. No. 6.1e-19;		
Matches	114; Conservative 0; Mismatches 19; Indels 1; Gaps 1;		
Oy	1	GCTCCCCCGCGTGTATGCAATGAGATGATAGAGGCTCGTGAGATTGACGTGAGGGG	60
Db	196	GCTTCCCGCGGTGATGCAATGAGATGATGATGAAGGCTCGTGAGATTGACTGAGGGGG	255
Oy	61	CAGGATATGCCTATA-TTCTGGAGCGAACTCCGGCGGAATACGAAGCCTTTGATACGT	119
Db	256	TAGGATATGCCTATATTCTTCGGAGCGAAGCTCAGGCGGAATATGAAGCGCATGATACAAG	315
Oy	120	TGTAGGAGGGGATT	133
Db	316	TTATGCCCTTGAAT	329
RESULT 3			
LOCUS	CN872595	498 bp	mRNA linear EST 04-JUN-2004
DEFINITION	020807AAPA005328RT (AAPA) Royal Gala 24 DABF fruit Malus x domestica cDNA clone AAPA005328, mRNA sequence.		

ACCESSION	CN872595
VERSION	CN872595.1 GI:48258753
KEYWORDS	EST.
SOURCE	Malus x domestica
ORGANISM	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
REFERENCE	1 (bases 1 to 498) Bennett, J., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B., Mortley, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y. HortResearch Apple EST Project Unpublished (2004)
TITLE	Contact: Gleave, A.
JOURNAL	Sequencing Facility The Horticulture and Food Research Institute of New Zealand Ltd 120 Mt Albert Rd, Mt Albert, Auckland, New Zealand Tel.: 00 64 09 815 4200 Fax: 00 64 09 815 4201 Email: est@hortresearch.co.nz.
COMMENT	Location/Qualifiers 1..498
FEATURES	/organism="Malus x domestica" /mol_type="mRNA" /db_xref="taxon:3750" /clone="AAPA005328" /ribose_type="fruit" /dev_stage="24 days after full bloom" /clone_id="(AAPA) Royal Gala 24 DAFB fruit" /note="Vector: PBK-CMV; Library sequenced by Genesis Research & Development"
ORIGIN	
Query Match	58.9%; Score 91.6; DB 7; Length 498;
Best Local Similarity	85.1%; Pred. No. 6.2e-19;
Matches 114; Conservative 0; Mismatches 19; Indels 1; Gaps 1;	
DQ	1 GCTCCCCCGGCGTTCATAGCATGATGAAGGCTGTGGATTGACGTAGGGG 60       
DB	247 GCTTCCCGGCCGTGATCGAAATGAAATGAAGATTAAGGCTGTGGATTGACGTAGGGG 306       
OY	61 CAGGGATGGGCATA-TTCTGGGAGCAACTCCGGCGCATATCAGAAGCGTTGATACGT 119       
DB	307 TAGGGAATGGCATATTTCTGGAGCGAACCTCACAGCATATGAAGCGCATGATACAG 366       
OY	120 TGTAGGAGCGGATT 133     
DB	367 TTATGCTTGGAAT 380     
RESULT 4	
AJ876197/c	510 bp mRNA linear EST 17-FEB-2005
LOCUS	AJ876197 Prunus persica fruit mesocarp plus epidermis 80 days after
DEFINITION	bloom Prunus persica cDNA clone PR0213A05, mRNA sequence.
ACCESSION	AJ876197
VERSION	AJ876197.1 GI:59932682
KEYWORDS	EST.
SOURCE	Prunus persica (peach)
ORGANISM	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Rosales; Rosaceae; Amygdaloidae; Prunus.
REFERENCE	1 (bases 1 to 510) Le Dater, L., Cosson, P., Renaud, C., Garcia, V., Dumoulin, P., Rochan, C., Filippi, G., Laigret, F., Moing, A. and Dirlewanger, E. Peach (Prunus persica (L.) Batsch) fruit ESTs from two early development stages
AUTHORS	Unpublished (2004)
TITLE	Contact: Le Dater, L.
JOURNAL	urefy, Inra, INRA, Centre de Bordeaux
COMMENT	BP 81 Villenave d'Ornon Cedex, 33 883, FRANCE. Location/Qualifiers
FEATURES	



DEFINITION PGAE30TF PGA Carica papaya genomic clone PGAE30, genomic survey sequence.  
 ACCESSION CG026604  
 VERSION CG026604.1 GI:33898760  
 KEYWORDS GSS.  
 SOURCE Carica papaya (papaya)  
 ORGANISM Carica papaya  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Caricaceae; Carica.  
 1 (bases 1 to 764)  
 Town, C.D., Van Aken, S., Utterback, T. and Fraese, C.M.  
 TITLE Whole genome shotgun sequencing of Carica papaya  
 JOURNAL Unpublished (2003)  
 COMMENT Other GSSs: PGAE30TR  
 CONTACT: Chris Town  
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtown@tigr.org  
 DNA provided by Ray Ming was isolated from cultivar Sundp that was transgenic for papaya ringspot virus coat protein gene  
 Seq primer: TF  
 Class: sheared ends.  
 Location/Qualifiers  
 1..764  
 /organism="Carica papaya"  
 /mol\_type="genomic DNA"  
 /cultivar="Sundp"  
 /db\_xref="taxon:3649"  
 /clone\_1ib="PGAE30"  
 /note="Vector: pHOS1, Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"

ORIGIN

Query Match 68.9%; Score 91.6; DB 10; Length 764;  
 Best Local Similarity 85.1%; Pred. No. 6,7e-19;  
 Matches 114; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGTTCATGATGATGATGAAGCGCTCGTGGATTGACGTGAGGGG 60  
 662 GCTCCCCCGCGTTCATGATGATGATGAAGCGCTCGTGGATTGACGTGAGGGG 603

DB 61 CAGGATGCGCTAAT-TTCTGGAGCGAATCCCGGCGCAATACGAAGCGCTTGATACAGT 119  
 602 TAGGGATGCGCTAATTTCTGGAGCGAATCCCGGCGCAATATGAAGCGCATGATACAG 543

QY 120 TGTAGGAGGAGATT 133  
 542 TTATGCTTGGAA 529

DB 542 TTATGCTTGGAA 529

RESULT 8  
 CK767400 610 bp mRNA linear EST 09-JUN-2005  
 LOCUS pam01-9ms1-a06 Persea americana cDNA clone pam01-9ms1-a06 5',  
 DEFINITION mRNA sequence.  
 ACCESSION CK767400  
 VERSION CK767400.1 GI:42721434  
 KEYWORDS EST.  
 SOURCE Persea americana (avocado)  
 ORGANISM Persea americana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae; Persea.  
 1 (bases 1 to 610)  
 dePamphilis, C., Carlson, J., Ma, H., Soltis, D., Soltis, P.,  
 Oppenheimer, D., Frohlich, M., Doyle, J., Tanksley, S., Webb, M.,  
 Leebens-Mack, J., Landherr, L., Ilut, D. and Wall, K.  
 TITLE Whole genome shotgun sequencing of Persea americana  
 JOURNAL Unpublished (2003)

COMMENT Contact: Claude dePamphilis or James Leebens-Mack  
 Mueller Laboratory  
 Penn State University  
 208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn  
 State University, University Park, PA 16802, USA  
 Tel: 814 863 6413  
 Fax: 814 865 9131  
 Email: cwt2@psu.edu or jh110@psu.edu  
 The sequence provided is trimmed of vector and low quality regions.  
 Full sequence and original trace file are available from the Plant  
 Genome Network website (<http://psn.cornell.edu>)  
 Plate: pam01-9ms1 row: a column: 06  
 Seq primer: M13F.

FEATURES  
 source  
 Location/Qualifiers  
 1..610  
 /organism="Persea americana"  
 /mol\_type="mRNA"  
 /db\_xref="PSC:pam01-9ms1-a06"  
 /db\_xref="taxon:3435"  
 /clone\_1ib="pam01-9ms1-a06"  
 /tissue\_type="flower buds"  
 /dev\_stage="12-20 mm buds"  
 /lab\_host="SOLR"  
 /clone\_1ib="pam01"  
 /note="Vector: pBluescript SK (+/-); site 1: EcoRI; site 2: XhoI; This is a directionally cloned, non-normalized library. This library has been generated by the Floral Genome Project (FGP). The Floral Genome Project is funded by NSF's Plant Genome Research Program (DBI-0115684). More information about the project can be obtained at <http://fgp.bio.psu.edu>"

ORIGIN

Query Match 68.6%; Score 91.2; DB 7; Length 610;  
 Best Local Similarity 85.6%; Pred. No. 8.7e-19;  
 Matches 113; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGTTCATGATGATGATGAAGCGCTCGTGGATTGACGTGAGGGG 60  
 48 GCTCCCCCGCGTTCATGATGATGATGAAGCGCTCGTGGATTGACGTGAGGGG 107

DB 61 CAGGATGCGCTAAT-TTCTGGAGCGAATCCCGGCGCAATACGAAGCGCTTGATACAGT 119  
 108 TAGGGATGCGCTAATTTCTGGAGCGAATCCCGGCGCAATATGAAGCGCATGATACAG 167

QY 120 TGTAGGAGGAGA 131  
 168 CTTGGAATGAA 179

DB 168 CTTGGAATGAA 179

RESULT 9  
 BH674012/c 839 bp DNA linear GSS 19-FEB-2002  
 LOCUS BOMHD96TR\_BO\_2.3 KB Brassica oleracea genomic clone BOMHD96,  
 DEFINITION genomic survey sequence.  
 ACCESSION BH674012  
 VERSION BH674012.1 GI:18742175  
 KEYWORDS GSS.  
 SOURCE Brassica oleracea  
 ORGANISM Brassica oleracea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 839)  
 Ayala, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,  
 Utterback, T.R., Mortman, J.R., White, O.R. and Town, C.D.  
 TITLE Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis  
 JOURNAL Genome Res. 15 (4), 487-495 (2005)  
 COMMENT PubMed 15805490  
 CONTACT: Chris Town  
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdcow@clgr.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TR  
 Class: sheared ends.

## FEATURES

## Source

Location/Qualifiers

1..839  
 /organism="Brassica oleracea"  
 /mol\_type="genomic DNA"  
 /strain="TOL1000DH3"  
 /db\_xref="taxon:3712"  
 /clone="BOKMD96"  
 /clone\_1lb="BO\_2\_3\_KB"  
 /note="Vector: pHOS1, Site 1: BstXI; 2-3 kb sheared  
 genomic DNA inserted into pHOS1 using BstXI linkers"

## ORIGIN

Query Match 68.4%; Score 91; DB 9; Length 839;  
 Best Local Similarity 80.9%; Pred. No. 1.1e-18;  
 Matches 106; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 3 TCCCCCGCGCTTCATGAGATGATAGAGCGCTGCGGATTCGTCGAGCGGCA 62  
 |||||  
 DB 828 TCTTCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 769  
 |||||  
 QY 63 GGGATGGCTATATTCCTGGAGCGAATCCGGGCGAATACGAAGCGCTTGATACAGTTGT 122  
 |||||  
 DB 768 GGGGAGTATATTCCTGGAGCGAATCCGATCGAATTCGATGAGCGCATACAGTTA 709  
 |||||  
 QY 123 AGGAGGAGATT 133  
 |||||  
 DB 708 TGACTTGGAAAT 698

## RESULT 10

## LOCUS

CN859023 380 bp mRNA linear EST 03-JUN-2004  
 000728AAAA00805HT (AAAA) Royal Gala 59 DAFB fruit, seeds removed

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## EST

## Malus x domestica

## Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

## Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

## Rosidae; eucosids I; Rosales; Rosaceae; Maloideae; Malus.

## 1 (bases 1 to 380)

## Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Jansen, B.,

## McArdney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.

## HortResearch Apple EST Project

## Unpublished (2004)

## Contact: Gleave, A.

## Sequencing Facility

## The Horticulture and Food Research Institute of New Zealand Ltd

## 120 Mt Albert Rd, Mt Albert, Auckland, New Zealand

## Tel: 00 64 09 815 4200

## Fax: 00 64 09 815 4201

## Email: est@hortresearch.co.nz.

## Location/Qualifiers

## 1..380

## /organism="Malus x domestica"

## /mol\_type="mRNA"

## /db\_xref="taxon:3750"

## /clone="AAAA00805"

## /tisue\_type="fruit"

## /dev\_stage="59 days after full bloom, seeds removed"

## /clone\_1lb="(AAAA) Royal Gala 59 DAFB fruit, seeds removed"

## /note="Vector: PBK-CMV; Library sequenced by Genesis Research &amp; Development"

## ORIGIN

Query Match 68.1%; Score 90.6; DB 7; Length 380;  
 Best Local Similarity 84.3%; Pred. No. 1.3e-18;  
 Matches 113; Conservative 0; Mismatches 20; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGCTTCATGAGATGATAGAGCGCTCGGAGTTGACGTGAGCGG 60  
 |||||  
 DB 245 GCTTCCCCCGCGCTATCGAATGATGATGATGATGATGATGATGATGATGATGATGAT 304  
 |||||  
 QY 61 CAGGATGGCTATA-TTCTGGAGCGAATCCGGGCGAATACGAAGCGCTTGATACAGT 119  
 |||||  
 DB 305 TAGGATGGCTATATTCCTGGAGCGAATCCGATCGAATATGAAAGCGCATGATACAG 364  
 |||||  
 QY 120 TGTAGGAGGAGATT 133  
 |||||  
 DB 365 TTATGCCCTTGAAT 378

## RESULT 11

## LOCUS

## BH009864/c

## DEFINITION

## eg27e02.x1 TOL1000 Brassica oleracea genomic clone eg27e02 5',

## genomic survey sequence.

## BH009864

## VERSION

## BH009864.1 GI:13956007

## KEYWORDS

## SSS.

## Brassica oleracea

## Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

## Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

## Rosidae; eucosids II; Brassicales; Brassicaceae; Brassica.

## 1 (bases 1 to 491)

## Katrari, M., O'Shaughnessy, A., Palmer, L., Bahret, A., Baker, J.,

## Ballis, V., Bell, M., Cummins, D.M., King, L., Kirchoff, K., Kuit, K.,

## Miller, B., Nascimento, L., Preston, R., Rodriguez, S., Santos, L.,

## Shah, R., Vil, M.D., Zuber, T., Bal, H., Dedina, N. and McCombie, W.R.

## Whole Genome Shotgun Reads from Brassica oleracea

## Unpublished (2001)

## Contact: W. Richard McCombie

## Lita Annenberg Hazen Genome Sequencing Center

## Cold Spring Harbor Laboratory

## PO Box 100, Cold Spring Harbor, NY 11724, USA

## Tel: 516 367 8884

## Fax: 516 367 8874

## Email: mccombie@cshl.org

## Plate: eg27 row: e column: 02

## Seq primer: -21fwduniv

## Class: Shotgun

## High quality sequence stop: 491.

## Location/Qualifiers

## 1..491

## /organism="Brassica oleracea"

## /mol\_type="genomic DNA"

## /db\_xref="taxon:3712"

## /clone="eg27e02"

## /clone\_1lb="TOL1000"

## /note="Vector: M13 for .x reads, pZero-2 for .b and .g reads; Site 1: BclRV; DNA prepared as whole genome shotgun library from young, green leaves. May contain some plasmid DNAs. DNA provided by Dr. Tom Osborn, University of Wisconsin-Madison, Department of Agronomy."

## ORIGIN

Query Match 64.2%; Score 85.4; DB 9; Length 491;  
 Best Local Similarity 85.6%; Pred. No. 6.6e-17;  
 Matches 95; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 GCTCCCCCGCGCTTCATGAGATGATAGAGCGCTCGGAGTTGACGTGAGCGG 60  
 |||||  
 DB 111 GCTCCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 52  
 |||||  
 QY 61 CAGGATGGCTATATTCCTGGAGCGAATCCGGGCGAATACGAAGCGCTTG 111  
 |||||

Db	51	TAGGGGTGCTATTATTATGGAGCACTCCATCGAATATGAAGCGATG	1
RESULT 12			
LOCUS	BZ511771	770 bp	DNA linear GSS 16-DEC-2002
DEFINITION	BOMQT22TR_BO_2_3_KB Brassica oleracea genomic clone BOMQT22.		
ACCESSION	BZ511771		
VERSION	BZ511771.1	GI:27037291	
KEYWORDS	GSS.		
SOURCE	Brassica oleracea		
ORGANISM	Brassica oleracea		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.		
AUTHORS	Ayala, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S., Utecherback, T.R., Mortman, J.R., White, O.R. and Town, C.D.		
TITLE	Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis		
JOURNAL	Genome Res. 15 (4), 487-495 (2005)		
PUBMED	15805490		
COMMENT	Other GSSs: BOMQT22RF Contact: Chris Town TIR		
FEATURES	7972 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523 Fax: 301-838-0208 Email: cdtown@tigr.org DNA is from a doubled haploid provided by Tom Osborn. Seq primer: TR Class: sheared ends. Location/Qualifiers 1..770 /organism="Brassica oleracea" /mol_type="genomic DNA" /strain="T01000DH3" /db_xref="taxon:3712" /clone="BOMQT22" /clone_1fb="BO_2_3_KB" /note="Vector: pHOST1, Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOST1 using BstXI linkers"		
ORIGIN			
Query Match	64.1%; Score 85.2; DB 9; Length 770;		
Best Local Similarity	82.1%; Pred. No. 8.2e-17;		
Matches 110; Conservative	0; Mismatches 23; Indels 1; Gaps 1;		
OY	1 GCTCCCCCGCCGCTTCATGAGATGATGAAGGCTCGTGGAGATTGACGTAGGGGG 60		
Db	5 GCTCCCTCGCTGTGATTGATTAAGATGAAGAGGCTCGTGGAGATTGACGTAGGGGG 64		
OY	61 CAGGGATGGCTATA-TTCTGGAGCGAAGCTCGGGCGAATCGAAGCGCTTGATACGT 119		
Db	65 TAGGGGTGCTATTATTCTGGAGCGAAGCTCCATCGAATATGAAGCGCATGATACAG 124		
OY	120 TGTAGGAGGAGATT 133		
Db	125 TTATGACTTGGAAT 138		
RESULT 13			
LOCUS	BH424823	775 bp	DNA linear GSS 12-DEC-2001
DEFINITION	BOHNU79TR_BOH Brassica oleracea genomic clone BOHNU79, genomic survey sequence.		
ACCESSION	BH424823		
VERSION	BH424823.1	GI:17610551	
KEYWORDS	GSS.		
SOURCE	Brassica oleracea		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		

REFERENCE	AUTHORS	TITLE	JOURNAL	PUBMED	COMMENT
1 (bases 1 to 775)	Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S., Utecherack,T.R., Wortman,J.R., White,O.R. and Town,C.D.	Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis Genome Res. 15 (4), 487-495 (2005)		15805490	
Other GSSs:	BOHNU79TF				
Contact:	Chris Town				
TIGR					
9712 Medical Center Drive, Rockville, MD 20850, USA.					
Tel: 301-838-3523					
Fax: 301-838-0208					
Email: cdtown@tigr.org					
DNA is from a doubled haploid provided by Tom Osborn.					
Seq primer: TR					
Class: sheared ends.					
Location/Qualifiers					
1. 775					
/organism="Brassica oleracea"					
/mol_type="genomic DNA"					
/strain="TO100DH3"					
/db_xref="taxon:3712"					
/clone="BOHNU79"					
/note="Vector: PHOS1; Site 1: BatXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BatXI linkers"					
ORIGIN					
Query Match	64.1%;	Score 85.2;	DB 9;	Length 775;	
Best Local Similarity	82.1%;	Prod. No. 8.2e-17;			
Matches 110;	Conservative 0;	Mismatches 23;	Indels 1;	Gaps 1;	
Oy	1	GCTCCCCCGCCGTCGTCATGGAATGAAATGAGAGCGCTGGGATGACGAGGCGG	60		
Db	11	GCTCCCTCGCTGTTGTGAATGAAGATGAAGAGCGCTGGGATGACGAGGCGG	70		
Oy	61	CAGGATGAGCATAT-TTCTGGAGCGAATCCCGGCGAATACGAAGCGCTGTGATACGT	119		
Db	71	TAGGGGATGCTATATTTCTGGAGCGAATCTCATGCAATATGAGCGCATGATACAG	130		
Oy	120	TGTAGGAGCGGATT	133		
Db	131	TTATGACTTGGAAAT	144		
RESULT 14					
BH957918		713 bp	DNA	linear	GSS 01-OCT-2002
LOCUS	odf85c05.b1	Brassica oleracea genomic,	genomic survey		
DEFINITION					
ACCESSION	BH957918				
VERSION	BH957918				
KEYWORDS	BH957918.1	GI:23439145			
SOURCE	GSS.				
ORGANISM	Brassica oleracea				
	Brassicaceae				
	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.				
	1 (bases 1 to 713)				
	Deleahunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T., Nash,W., Rabinowicz,P.D. and Wilson,R.K.				
	Whole genome shotgun reads from Brassica oleracea				
	Unpublished (2002)				
	Contact: Richard K. Wilson				
	Genome Sequencing Center				
	Washington University School of Medicine				
	Email: submissions@watson.wustl.edu				
	Plate: odf85	row: C	column: 05		
	Seq primer: -21UPOT	forward			
	Class: shotgun				

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/clone lib="BO_1.6.2_KB_tot"
/notes="Vector: pHOSt_Site 1: BstXI: 1.6-2 kb sheared"
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Search completed: April 18, 2006, 01:01:36  
Job time : 2983 secs

11115 rage Blank (uspto)

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 17, 2006, 23:31:51 ; Search time 485 Seconds  
(without alignments)  
1827.637 Million cell updates/sec

Title: US-10-663-241-32

Perfect score: 133  
Sequence: 1 gctcccccgcgcgtcgttca.....tacagtcgaggagggatt 133

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_21.\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	133	100.0	133	2	AAV9599 Prm PEP
2	122	91.7	165	2	AAx21409
3	122	91.7	168	2	AAx21407
4	122	91.7	176	12	ADM01282
5	122	91.7	1134	2	AAx21415
6	122	91.7	1134	2	AAx21415
7	122	91.7	1143	10	ADe06202
8	122	91.7	1148	12	ADe085784
9	122	91.7	1332	12	ADe085782
10	122	91.7	1416	2	AAx21432
11	122	91.7	1417	2	AAx21432
12	122	91.7	1417	10	ADe06203
13	122	91.7	5834	12	ADM01283
14	122	91.7	6465	12	ADM01293
15	122	91.7	6659	12	ADM01290
16	122	91.7	7549	12	ADM01292
17	121	91.0	161	2	AAx21423
18	121	91.0	1183	3	AAx21376
19	121	91.0	1208	2	AAx21433

20	121	91.0	1613	12	ADe085788	ADe085788 ChimERIC
21	121	91.0	1920	13	ADR70709	ADR70709 DNA const
22	121	91.0	2145	8	ABx13738	Abx13738 Edited St
23	121	91.0	4671	3	AAx21385	AAx21385 Nucleotid
24	119.4	89.8	1544	8	ABx13719	Abx13719 pSAC114 v
25	119.4	89.8	2391	8	ABx13737	Abx13737 Scryptomy
26	118.8	89.3	150	2	AAx21406	AAx21406 Prtm/psba
27	117.8	88.6	4591	6	ABx55360	ABx55360 DNA seque
28	114.8	86.3	142	6	ABx55361	ABx55361 Nicotiana
29	107	80.5	119	14	ADx17034	Adx17034 Tobacco 1
30	102.8	77.3	184	4	AAx89143	AAx89143 Tobacco p
31	102.8	77.3	201	2	AAx16301	AAx16301 DNA of up
32	102.8	77.3	220	6	ABx54934	ABx54934 DNA seque
33	102.8	77.3	233	13	ADT78239	ADT78239 Tobacco p
34	102.8	77.3	2569	12	ADT05018	ADT05018 alpha-6/np
35	102.8	77.3	2962	2	AAx21408	AAx21408 targetin
36	102.8	77.3	3204	12	ADT05016	ADT05016 aada/BADH
37	102.8	77.3	3300	12	ADT05017	ADT05017 gfp/BADH
38	102.8	77.3	4363	9	ACC85346	ACC85346 PCB42-94
39	102.8	77.3	4363	10	ADx34324	ADx34324 Plastid t
40	102.8	77.3	4363	12	ADx01707	ADx01707 Tobacco c
41	102.8	77.3	4746	10	ADx34240	ADx34240 Plastid p
42	102.8	77.3	6477	5	AAx16797	AAx16797 Chloropla
43	102.8	77.3	7652	12	ADx007359	ADx007359 Plastid t
44	102.8	77.3	8684	12	ADx007360	ADx007360 Plastid t
45	102.8	77.3	10011	12	ADx007377	ADx007377 Plastid t

ALIGNMENTS

RESULT 1	AAV9599 standard; DNA; 133 BP.
ID	AAV9599
XX	AAV9599;
AC	27-AUG-2003 (revised)
DT	29-MAR-1999 (first entry)
XX	Prm PEP promoter.
DE	Promoter; nuclear encoded plastid RNA polymerase; NEP;
XX	KW Plastid encoded plastid RNA polymerase; PEP; Prm; chloroplast;
KW	transgenic plant; maize; ss.
XX	Unidentified.
OS	WO9855595-A1.
XX	10-DEC-1998.
PD	03-JUN-1998; 98WO-US011437.
PF	03-JUN-1997; 97US-0048376P.
XX	12-SEP-1997; 97US-0058670P.
PR	(RUTP ) UNIV RUTGERS STATE NEW JERSEY.
PA	Malgia P, Silhavy D, Sritaman P;
PI	WPI; 1999-070262/06.
DR	Isolated nuclear-encoded plastid RNA polymerase promoter sequences -
PT	useful for expressing exogenous protein in plant plastids such as
PT	chloroplasts.
PT	Disclosure; Page 4; 79pp; English.
PS	This is the nucleotide sequence of plasmid-encoded plastid RNA polymerase
XX	(PEP) Prm promoter. Isolated rpoB, acpB, cnp and 16S rDNA promoter
CC	elements (see AAV9599-99) or homologues are used for producing exogenous
CC	proteins of interest in plant plastids. Also new is a DNA construct for

CC stably transforming the plasmids of higher plants comprising: (i) a  
CC transcription unit encoding at least one exogenous protein of interest,  
CC and (ii) a first nuclear-encoded plastid (NEP) RNA polymerase promoter,  
CC and a second NEP RNA polymerase promoter in tandem operably linked to the  
CC transcription unit, where expression of the transcription unit is  
CC regulated by the promoters. Use of the novel constructs facilitates  
CC transformation of a wide range of plant species, allowing ubiquitous  
CC expression of a transforming DNA in plastids (e.g. chloroplasts) of  
CC multicellular plants. Preferred promoter combinations are the Prn1 NEP  
CC promoters combined with clp type II NEP promoter in dicots and the Prn1  
CC NEP promoter combined with the clp type II NEP promoter in monocots and  
CC dicots. (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 133 BP; 30 A; 25 C; 50 G; 28 T; 0 U; 0 Other;

Query Match 100.0%; Score 133; DB 2; Length 133;

Best Local Similarity 100.0%; Pred. No. 3.2e-37; Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCCCGCCGCTGTTCAATGAGATGATGATGAGGCTGTTGATTCAGCTGAGGGG 60  
DB 1 GCTCCCGCCGCTGTTCAATGAGATGATGATGAGGCTGTTGATTCAGCTGAGGGG 60

QY 61 CAGGATGGCTATATTCTGGGAGCGAATCTCCGGCGAATGCAAGCGCTTGATACAGTT 120  
DB 61 CAGGATGGCTATATTCTGGGAGCGAATCTCCGGCGAATGCAAGCGCTTGATACAGTT 120

QY 121 GTAGGAGGGATT 133  
DB 121 GTAGGAGGGATT 133

RESULT 2  
AAX21409

ID AAX21409 standard; DNA; 165 BP.

XX AAX21409;

DT 21-MAY-1999 (first entry)

XX Prn1 promoter sequence.

KM Construct; marker; antibiotic resistance; regulatory sequence; promoter;  
KM stabilizing sequence; plastid; plant; ss.

XX Synthetic.

OS Nicotiana tabacum.

XX US5877402-A.

XX 02-MAR-1999.

XX 31-JAN-1994; 94US-00189256.

XX 01-MAY-1990; 90US-00518763.

XX 25-AUG-1993; 93US-00111398.

PA (RUTP ) UNIV RUTGERS STATE NEW JERSEY.

XX Maliga ZS, Maliga P, Staub JM;

XX WPI; 1999-189744/16.

PT New DNA construct containing an antibiotic resistance marker - useful for  
PT stably transforming the plastids of multicellular plants.

XX Disclosure; Fig 18A; 101pp; English.

CC The invention relates to a DNA construct, containing a non-lethal stable  
CC marker (e.g. antibiotic resistance) under the control of a 5' regulatory  
CC sequence and a 3' stabilizing sequence, for stably transforming the  
CC plastids of multicellular plants and allowing expression of heterologous  
CC proteins especially non-native plastid or plant proteins. This sequence

CC corresponds to the 16S ribosomal RNA operon promoter (Prn1)  
XX Sequence 165 BP; 40 A; 31 C; 61 G; 33 T; 0 U; 0 Other;

QY Query Match 91.7%; Score 122; DB 2; Length 165;  
Best Local Similarity 99.3%; Pred. No. 2.9e-33;  
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GTCCTCCCGCCGCTGTTCAATGAGATGATGATGAGGCTGTTGATTCAGCTGAGGGG 60  
DB 1 GTCCTCCCGCCGCTGTTCAATGAGATGATGATGAGGCTGTTGATTCAGCTGAGGGG 60

QY 61 CAGGATGGCTATA-TTCTGGAGGCGAATCTCCGGCGAATGCAAGCGCTTGATACAGT 119  
DB 61 CAGGATGGCTATA-TTCTGGAGGCGAATCTCCGGCGAATGCAAGCGCTTGATACAGT 120

QY 120 TGTAGGAGGGATT 133  
DB 121 TGTAGGAGGGATT 134

RESULT 3

ID AAX21407 standard; DNA; 168 BP.

XX AAX21407;

DT 21-MAY-1999 (first entry)

XX Prn1/rbcl/Rubisco regulatory region.

KM Construct; marker; antibiotic resistance; regulatory sequence; promoter;  
KM stabilizing sequence; plastid; plant; ss.

XX Synthetic.

OS Nicotiana tabacum.

XX US5877402-A.

XX 02-MAR-1999.

XX 31-JAN-1994; 94US-00189256.

XX 01-MAY-1990; 90US-00518763.

XX 25-AUG-1993; 93US-00111398.

PA (RUTP ) UNIV RUTGERS STATE NEW JERSEY.

XX Maliga ZS, Maliga P, Staub JM;

XX WPI; 1999-189744/16.

PT New DNA construct containing an antibiotic resistance marker - useful for  
PT stably transforming the plastids of multicellular plants.

XX Disclosure; Fig 8; 101pp; English.

CC The invention relates to a DNA construct, containing a non-lethal stable  
CC marker (e.g. antibiotic resistance) under the control of a 5' regulatory  
CC sequence and a 3' stabilizing sequence, for stably transforming the  
CC plastids of multicellular plants and allowing expression of heterologous  
CC proteins especially non-native plastid or plant proteins. This sequence  
CC corresponds to the regulatory region of the plasmid pTNH32 and comprises  
CC the 16S ribosomal RNA operon promoter (Prn1) the rbcl leader sequence  
CC including the ribosome binding site and the first 5 amino acids coding  
CC sequence from the ribosome-1,5-bisphosphate decarboxylase/oxygenase large  
CC subunit (Rubisco) gene

XX Sequence 168 BP; 44 A; 32 C; 57 G; 35 T; 0 U; 0 Other;

Query Match 91.7%; Score 122; DB 2; Length 168;

Best Local Similarity 99.3%; Pred. No. 2.9e-33; Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGTCGTTCAATGAGATGATTAAGAGCGTCGTGGATTGACGTGAGGGG 60  
 Db 1 GCTCCCCCGCGTCGTTCAATGAGATGATTAAGAGCGTCGTGGATTGACGTGAGGGG 60  
 QY 61 CAGGAGTGGCTATAT-TTCTGGAGCGGAATCTCCGGCGAATACGAAGCGCTTGATACAGT 119  
 Db 61 CAGGAGTGGCTATATTTCTGGAGCGGAATCTCCGGCGAATACGAAGCGCTTGATACAGT 120  
 QY 120 TGTAGGAGGAGATT 133  
 Db 121 TGTAGGAGGAGATT 134  
 RESULT 4  
 ADM01282  
 ID ADM01282 standard; DNA; 176 BP.  
 AC ADM01282;  
 DT 01-JUL-2004 (first entry)  
 DE Plasmid 16S ribosomal RNA subunit promoter sequence.  
 XX vector; plasmid; artificial intergene region; plant;  
 KW transplastomic angiosperm; agronomic property; stress resistance;  
 KM rbcL gene; ds.  
 XX Unidentified.  
 OS  
 PN WO2004029256-A2.  
 PD 08-APR-2004.  
 PF 15-SEP-2003; 2003WO-CU000009.  
 PR 27-SEP-2002; 2002CU-00000208.  
 PA (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.  
 PI Selman-Housein Sosa G, Aguilar Cabeza E, Gonzalez Quintero ADC;  
 PI Ramos Gonzalez O;  
 DR WPI; 2004-316131/29.  
 PT DNA vector for transformation and expression in plasmids, useful e.g. for  
 PT producing pharmaceutical proteins or improving agronomic properties, has  
 PT gene inserted in artificial intergene region.  
 PS Example 1; SEQ ID NO 14; 74pp; Spanish.  
 XX The invention relates to a DNA vector (A) for stable transformation and  
 CC expression of genes (I) in plasmids, where (I) is inserted in an  
 CC artificial intergene region (AIR) formed by combining two 5'-untranslated  
 CC regions (5'-UTRs) of genes that transcribe in different directions and  
 CC are derived from plants of different divisions or classes. (A) are used  
 CC to produce transplastomic angiosperms that have improved agronomic  
 CC properties (e.g. resistance to biotic or abiotic stress) or express a  
 CC very wide range of agricultural, veterinary, pharmaceutical, nutritional  
 CC or industrial products, e.g. enzymes, vaccinating antigens, cytokines or  
 CC immunoglobulins. Use of (A) eliminates the need for a transposon for gene  
 CC insertion; inserted genes do not require promoters and terminators; and  
 CC the structure of flanking sequences in (A) ensures universal  
 CC applicability. Also any selection marker in (A) can be eliminated by  
 CC homologous recombination. (A) provides efficient and stable expression of  
 CC genes without causing any functional alterations. This sequence  
 CC represents the plasmid 16S ribosomal RNA subunit promoter sequence used  
 CC to generate the vectors of the invention.  
 SQ Sequence 176 BP; 39 A; 37 C; 60 G; 40 T; 0 U; 0 Other;  
 Query Match 91.7%; Score 122; DB 12; Length 176;  
 Best Local Similarity 99.3%; Pired. No. 2.9e-33;

Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 GCTCCCCCGCGTCGTTCAATGAGATGATTAAGAGCGTCGTGGATTGACGTGAGGGG 60  
 Db 16 GCTCCCCCGCGTCGTTCAATGAGATGATTAAGAGCGTCGTGGATTGACGTGAGGGG 75  
 QY 61 CAGGAGTGGCTATAT-TTCTGGAGCGGAATCTCCGGCGAATACGAAGCGCTTGATACAGT 119  
 Db 76 CAGGAGTGGCTATATTTCTGGAGCGGAATCTCCGGCGAATACGAAGCGCTTGATACAGT 135  
 QY 120 TGTAGGAGGAGATT 133  
 Db 136 TGTAGGAGGAGATT 149  
 RESULT 5  
 AAT85195/c  
 ID AAT85195 standard; DNA; 1134 BP.  
 AC AAT85195;  
 DT 10-MAR-1998 (first entry)  
 DE Plasmid targeting region of plasmid pGS31A.  
 XX Plasmid; transformation; transplastomic plant; transgenic plant;  
 KW Brassica; cruciferous plant; vector; plasmid pGS31A.  
 KM spectinomycin resistance; selectable marker; aadA gene; ss.  
 XX Arabidopsis thaliana.  
 OS Synthetic.  
 OS Chimeric.  
 OS  
 PN WO9732977-A1.  
 PD 12-SEP-1997.  
 PF 06-MAR-1997; 97WO-US003444.  
 PR 06-MAR-1996; 96US-0012916P.  
 PA (RUTG) UNIV RUTGERS STATE NEW JERSEY.  
 PI Maliga P, Sikdar SR, Reddy SV;  
 PI WPI; 1997-470543/43.  
 PT Production of transplastomic plants - by transfection with plasmid  
 PT targeted DNA, specifically for Cruciferous plants.  
 PS Disclosure; Fig 6; 45pp; English.  
 XX This sequence comprises the plasmid targeting region of plasmid pGS31A.  
 CC This plasmid carries a spectinomycin resistance gene (aadA) flanked by  
 CC Arabidopsis plasmid DNA sequences that target its insertion between trnV  
 CC and the rps 12/7 operon. It was produced by ligating the chimeric aadA  
 CC gene from Ecol1236II into the unique HincII site of plasmid pGS7 (see  
 CC AAT85194). A novel method of production of transplastomic plants  
 CC involves: delivering transforming DNA, preferably cloned in pGS31A,  
 CC pGS85A or pGS7, to a plasmid genome of plant cells in culture, selecting  
 CC cells with transformed plasmids and regenerating these to plants. The  
 CC transforming DNA comprises (i) (i) several targeting sequences (i.e.  
 CC plasmid DNA sequences from the genome to be transformed) to allow  
 CC homologous recombination. (ii) 5' and 3' regulatory regions from plasmid  
 CC DNA linked to an antibiotic resistance gene for use as selection marker,  
 CC (iii) similar regulatory regions controlling a foreign gene of interest,  
 CC and (iv) at least one cloning site for insertion of the foreign gene  
 CC adjacent to the marker gene. The method is used to transform cruciferous  
 CC plants, e.g. Brassica species. The combination of homologous  
 CC recombination, selectable marker and use of plasmid regulatory sequences  
 CC improves generation of stably transformed plants. Expression of foreign  
 CC genes in plasmids, rather than in the nucleus, avoids risk of  
 CC transmitting the foreign gene in the pollen, provides high levels of

CC protein expression, permits simultaneous incorporation of several genes  
CC and avoids the positional effects and gene silencing associated with  
CC nuclear transformation

XX Sequence 1134 BP; 295 A; 310 C; 248 G; 281 T; 0 U; 0 Other;

Query Match 91.7%; Score 122; DB 2; Length 1134;  
Best Local Similarity 99.3%; Pred. No. 5.2e-33;  
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGTCCCCCGCGCTTCATATGAGATGATTAAGAGCTCTGGGATTGACGTGAGGGGG 60

DB 1130 GGTCCCCCGCGCTTCATATGAGATGATTAAGAGCTCTGGGATTGACGTGAGGGGG 1071

QY 61 CAGGATGGCTATTA-TTCTGGAGCGAACTCCGGCGGAATACGAACGCTTGATACACT 119

DB 1070 CAGGATGGCTATTA-TTCTGGAGCGAACTCCGGCGGAATACGAACGCTTGATACACT 1011

QY 120 TGTAGGAGGAGATT 133

DB 1010 TGTAGGAGGAGATT 997

RESULT 6

AAAX21415/c

ID AAAX21415 standard; DNA; 1134 BP.

AC AAAX21415;

DT 21-MAY-1999 (first entry)

DE Selectable marker gene for plasmid pPRV112A.

KW Construct; marker; antibiotic resistance; regulatory sequence; promoter;

XX stabilizing sequence; plasmid; plant; ss.

OS Synthetic.

PN US5877402-A.

PP 02-MAR-1999.

PR 31-JAN-1994; 94US-00189256.

PR 01-MAY-1990; 90US-00518763.

PR 25-AUG-1993; 93US-00111398.

PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.

PI Maliqa ZS, Maliqa P, Staub JM;

PI WPI, 1999-189744/16.

PT New DNA construct containing an antibiotic resistance marker - useful for

PT stably transforming the plasmids of multicellular plants.

PS Claim 21; Fig 20E; 101bp; English.

CC The invention relates to a DNA construct, containing a non-lethal stable

CC marker (e.g. antibiotic resistance) under the control of a 5' regulatory

CC sequence and a 3' stabilizing sequence, for stably transforming the

CC plasmids of multicellular plants and allowing expression of heterologous

CC proteins especially non-native plasmid or plant proteins. This sequence

CC corresponds to the selectable marker gene for the plasmid pPRV112A

XX Sequence 1134 BP; 291 A; 303 C; 257 G; 283 T; 0 U; 0 Other;

SO Query Match 91.7%; Score 122; DB 2; Length 1134;

Best Local Similarity 99.3%; Pred. No. 5.2e-33;

Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGTCCCCCGCGCTTCATATGAGATGATTAAGAGCTCTGGGATTGACGTGAGGGGG 60

DB 1058 GGTCCCCCGCGCTTCATATGAGATGATTAAGAGCTCTGGGATTGACGTGAGGGGG 999

QY 61 CAGGATGGCTATTA-TTCTGGAGCGAACTCCGGCGGAATACGAACGCTTGATACACT 119

DB 998 CAGGATGGCTATTA-TTCTGGAGCGAACTCCGGCGGAATACGAACGCTTGATACACT 939

QY 120 TGTAGGAGGAGATT 133

DB 938 TGTAGGAGGAGATT 925

RESULT 7

AADE06202/c

ID AADE06202 standard; DNA; 1143 BP.

AC AADE06202;

DT 29-JAN-2004 (first entry)

DE Nicotiana tabacum targeting region of plasmid pGS31A.

KW Vector; pZS391B; plasmid transformation; higher plant; transgene;

XX Brassica plant; transplasmomic plant; DNA delivery; targeting region;

XX plasmid pGS31A; plant; ds.

OS Nicotiana tabacum.

PN US2003200568-A1.

PP 12-JUN-2003; 2003US-00460716.

PR 06-MAR-1997; 97WO-US003444.

PR 05-FEB-1999; 98US-00142114.

PR 13-MAR-2000; 2000US-00524087.

PA (MALI/) MALIGA P.

PA (SKAR/) SKARJINSKAIA M.

PA (MALI/) MALIGA Z S.

PI Maliqa P, Skarjinskaia M, Maliqa ZS;

PI WPI, 2003-852834/79.

PT New improved vector for transforming plasmids of higher plants and

PT comprising a targeting segment having first and second chimeric targeting

PT sequences, useful for creating transplasmomic plants.

PS Disclosure; SEQ ID NO 2; 35bp; English.

CC The present invention relates to a new improved vector (pZS391B) for

CC transforming plasmids of higher plants. The vector comprises a targeting

CC segment having first and second chimeric targeting sequences for

CC facilitating recombination within the plasmid genome, each of which

CC flanks at least one transgene of interest and has a first portion derived

CC from the plant species being targeted for transformation, and a second

CC portion derived from a different plant species. The transgene constitutes

CC a monocistronic or polycistronic expression unit comprising a selectable

CC marker gene and a foreign gene of interest. It encodes a selectable

CC marker, herbicide resistance or drought resistance gene. The selectable

CC marker gene comprises kanamycin, streptomycin or spectinomycin. The

CC plasmids are chloroplasts. The vector is useful for transforming plasmids

CC of higher plants (e.g. Brassica plants), and for creating transplasmomic

CC plants. The methods and compositions of the invention facilitate the

CC regeneration of transformed plants following the delivery of beneficial

CC DNA molecules. The present sequence represents Nicotiana tabacum

XX targeting region of plasmid pGS31A.

SO Query Match 91.7%; Score 122; DB 10; Length 1143;

Best Local Similarity 99.3%; Pred. No. 5.2e-33;

Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGTCCCCCGCGCTTCATATGAGATGATTAAGAGCTCTGGGATTGACGTGAGGGGG 60

Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGTCTCATGAGATGATGAAGAGCTCGTGGATTGACGTAGGGGG 60  
DB 1130 GCTCCCCCGCGTCTCATGAGATGATGAAGAGCTCGTGGATTGACGTAGGGGG 1071

QY 61 CAGGGATGGCTATATTTCTGGAGAGCGAATCCGGGCGAATACGAAGCGCTTGATACAGT 119  
DB 1070 CAGGGATGGCTATATTTCTGGAGAGCGAATCCGGGCGAATACGAAGCGCTTGATACAGT 1011

QY 120 TGTAGGAGGGGATT 133  
DB 1010 TGTAGGAGGGGATT 997

## RESULT 8

AD085784  
ID AD085784 standard; DNA; 1148 BP.  
AC AD085784;  
XX  
XX  
DT 09-SEP-2004 (first entry)  
XX  
XX Chimeric gene AADA-129 SEQ ID NO:3.  
XX  
XX ds; gene; elementary chimeric gene; hydroxyphenyl pyruvate dioxygenase;  
KM HPPD; plant; weed control; herbicide.  
XX  
XX Nicotiana tabacum.  
OS Chimeric.

XX Key Location/Qualifiers  
FH CDS 136..930  
FT /\*tag= a  
FT /product= "AADA-129"

PN FR2848568-A1.

PD 18-JUN-2004.

PF 17-DEC-2002; 2002FR-00015975.

PR 17-DEC-2002; 2002FR-00015975.

PA (RHOB-) RHOBIO SA.

PI Tisot G, Wisniewski JP, Ferullo JM;

XX WPI; 2004-452915/43.

DR P-PSDB; AD085785.

XX  
XX  
XX New chimeric gene including a sequence for hydroxyphenyl pyruvate  
PT dioxygenase, useful for preparing transgenic plants resistant to  
PT herbicides that target this enzyme, by plastid transformation.

XX Example 1; SEQ ID NO 3; 47pp; French.

XX  
XX The invention relates to a novel chimeric gene (CG) comprising at least  
CC one elementary chimeric gene (ecG) that consists of, functionally linked  
CC in the direction of transcription, a promoter (P), functional in plants,  
CC a sequence encoding hydroxyphenyl pyruvate dioxygenase (HPPD) and a  
CC terminator, functional in plants. The chimeric genes of the invention are  
CC used to impart resistance to herbicides that target HPPD, so that plants  
CC containing CG can be safely treated, for weed control, with these  
CC herbicides. Plastid transformation, which involves a double homologous  
CC recombination, is precisely targeted, avoiding positional effects that  
CC occur during nuclear transgenesis. The present sequence represents an  
CC elementary chimeric gene of the invention.

XX  
SQ Sequence 1148 BP; 314 A; 256 C; 307 G; 271 T; 0 U; 0 Other;

Query Match 91.7%; Score 122; DB 12; Length 1148;  
Best Local Similarity 99.3%; Pred. No. 5; 2e-33;

Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGTCTCATGAGATGATGAAGAGCTCGTGGATTGACGTAGGGGG 60  
DB 1 GCTCCCCCGCGTCTCATGAGATGATGAAGAGCTCGTGGATTGACGTAGGGGG 60

QY 61 CAGGGATGGCTATATTTCTGGAGAGCGAATCCGGGCGAATACGAAGCGCTTGATACAGT 119  
DB 61 CAGGGATGGCTATATTTCTGGAGAGCGAATCCGGGCGAATACGAAGCGCTTGATACAGT 120

QY 120 TGTAGGAGGGGATT 133  
DB 121 TGTAGGAGGGGATT 134

## RESULT 9

AD085782  
ID AD085782 standard; DNA; 1332 BP.  
AC AD085782;  
XX  
XX  
DT 09-SEP-2004 (first entry)  
XX  
XX Chimeric gene AADA-111 SEQ ID NO:1.  
XX  
XX ds; gene; elementary chimeric gene; hydroxyphenyl pyruvate dioxygenase;  
KM HPPD; plant; weed control; herbicide.  
XX  
XX Nicotiana tabacum.  
OS Chimeric.

XX Key Location/Qualifiers  
FH CDS 136..930  
FT /\*tag= a  
FT /product= "AADA-111"

PN FR2848568-A1.

PD 18-JUN-2004.

PF 17-DEC-2002; 2002FR-00015975.

PR 17-DEC-2002; 2002FR-00015975.

PA (RHOB-) RHOBIO SA.

PI Tisot G, Wisniewski JP, Ferullo JM;

XX WPI; 2004-452915/43.

DR P-PSDB; AD085783.

XX  
XX  
XX New chimeric gene including a sequence for hydroxyphenyl pyruvate  
PT dioxygenase, useful for preparing transgenic plants resistant to  
PT herbicides that target this enzyme, by plastid transformation.

XX Example 1; SEQ ID NO 1; 47pp; French.

XX  
XX The invention relates to a novel chimeric gene (CG) comprising at least  
CC one elementary chimeric gene (ecG) that consists of, functionally linked  
CC in the direction of transcription, a promoter (P), functional in plants,  
CC a sequence encoding hydroxyphenyl pyruvate dioxygenase (HPPD) and a  
CC terminator, functional in plants. The chimeric genes of the invention are  
CC used to impart resistance to herbicides that target HPPD, so that plants  
CC containing CG can be safely treated, for weed control, with these  
CC herbicides. Plastid transformation, which involves a double homologous  
CC recombination, is precisely targeted, avoiding positional effects that  
CC occur during nuclear transgenesis. The present sequence represents an  
CC elementary chimeric gene of the invention.

XX  
SQ Sequence 1332 BP; 341 A; 272 C; 329 G; 390 T; 0 U; 0 Other;

Query Match 91.7%; Score 122; DB 12; Length 1332;  
Best Local Similarity 99.3%; Pred. No. 5; 4e-33;

Matches	133;	Conservative	0;	Mismatches	0;	Indels	1;	Gaps	2;
OY	1	GCTCCCCCGCGTGGTTCATGATGATGATTAAGAGCGCTCGTGGATTGACGTGAGGGG	60						
Db	1	GCTCCCCCGCGTGGTTCATGATGATGATTAAGAGCGCTCGTGGATTGACGTGAGGGG	60						
OY	61	CAGGATGGCTATATTCTGGAGAGCACTCCGGCGGATTAAGAACGCTTGATACGT	119						
Db	61	CAGGATGGCTATATTCTGGAGAGCACTCCGGCGGATTAAGAACGCTTGATACGT	120						
OY	120	TGTAGGAGGGATT	133						
Db	121	TGTAGGAGGGATT	134						
RESULT 10									
ID	AAAX21432	standard; DNA; 1416 BP.							
XX	AAAX21432;								
XX	AAAX21432;								
DT	21-MAY-1999	(first entry)							
XX									
XX									
DE	Regulatory region Prm(L)/rbcl(S)/kan/Tpsba(L).								
XX									
KX	Construct; marker; antibiotic resistance; regulatory sequence; promoter;								
KW	stabilizing sequence; plasmid; plant; ss.								
XX									
OS	Synthetic.								
XX									
PN	US5877402-A.								
PD	02-MAR-1999.								
XX									
PF	31-JAN-1994;	94US-00189256.							
XX									
PR	01-MAY-1990;	90US-00518763.							
PR	25-AUG-1993;	93US-00111398.							
XX									
PA	(RUTE ) UNIV RUTGERS STATE NEW JERSEY.								
PI									
PI	Maliqa ZS, Maliqa P, Staud JW;								
DR	WPI; 1999-189744/16.								
XX									
PT	New DNA construct containing an antibiotic resistance marker - useful for								
PT	stably transforming the plasmids of multicellular plants.								
XX									
PS	Disclosure; Fig 26A; 101pp; English.								
XX									
CC	The invention relates to a DNA construct, containing a non-lethal stable								
CC	marker (e.g antibiotic resistance) under the control of a 5' regulatory								
CC	sequence and a 3' stabilizing sequence, for stably transforming the								
CC	plasmids of multicellular plants and allowing expression of heterologous								
CC	proteins especially non-native plasmid or plant proteins. This sequence								
CC	corresponds to the regulatory region Prm(L)/rbcl(S)/kan/Tpsba(L) from								
CC	the plasmid pRMT7								
XX									
SQ	Sequence 1416 BP; 312 A; 322 C; 379 G; 403 T; 0 U; 0 Other;								
OY	Query Match	91.7%;	Score 122;	DB 2;	Length 1416;				
Db	Best Local Similarity	99.3%;	Pred. No. 5.5e-33;						
OY	Matches 133;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1				
OY	1	GCTCCCCCGCGTGGTTCATGATGATGATTAAGAGCGCTCGTGGATTGACGTGAGGGG	60						
Db	22	GCTCCCCCGCGTGGTTCATGATGATGATTAAGAGCGCTCGTGGATTGACGTGAGGGG	81						
OY	61	CAGGATGGCTATATTCTGGAGAGCACTCCGGCGGATTAAGAACGCTTGATACGT	119						
Db	82	CAGGATGGCTATATTCTGGAGAGCACTCCGGCGGATTAAGAACGCTTGATACGT	141						
OY	120	TGTAGGAGGGATT	133						

Db	142	TGTAAGGAGGATT	155
RESULT 11			
ID	AAAT85196		
XX	AAAT85196 standard; DNA; 1417 BP.		
AC	AAAT85196;		
DT	10-MAR-1998 (first entry)		
XX			
DE	Plastid targeting region of plasmid pGS85A.		
KM	Plastid; transformation; transplastomic plant; transgenic plant;		
KM	Brassica; cruciferous plant; vector; plasmid pGS85A;		
KM	kanamycin resistance; neomycin phosphotransferase; neo gene;		
KM	selectable marker; ss.		
XX			
OS	Arabidopsis thaliana.		
OS	Synthetic.		
XX	Chimeric.		
XX			
FT	Key	Location/Qualifiers	
FT	CDS	158..970	
FT		/tag= a	
FT		/note= "kanamycin resistance gene"	
XX			
XX	W09732977-A1.		
XX			
PD	12-SEP-1997.		
XX			
PF	06-MAR-1997; 97MO-US003444.		
XX			
PR	06-MAR-1996; 96US-0012916P.		
PA	(RUTP ) UNIV RUTGERS STATE NEW JERSEY.		
XX			
PI	Maliga P, Sikdar SR, Reddy SV;		
XX			
PI	WPI; 1997-470543/43.		
XX			
PT	Production of trans:plastomic plants - by transfection with plastid		
PT	targeted DNA, specifically for Cruciferous plants.		
XX			
PS	Disclosure; Fig 7; 45pp; English.		
XX			
CC	This sequence comprises the plastid targeting region of plasmid pGS85A.		
CC	This plasmid carries a neomycin phosphotransferase (neo) gene that		
CC	confers kanamycin resistance gene, flanked on both sides by Arabidopsis		
CC	plastid targeting sequences. It was produced by ligating the neo gene		
CC	into the unique HincII site of plasmid pGS7 (see AAAT85196). A novel		
CC	method of producing transplastomic plants involves: delivering		
CC	transforming DNA, preferably cloned in pGS31A, pGS85A or pGS7, to a		
CC	plastid genome of plant cells in culture, selecting cells with		
CC	transformed plastids and regenerating these to plants. Transforming DNA		
CC	comprises (i) (i) several targeting sequences (i.e. plastid DNA		
CC	sequences from the genome to be transformed) to allow homologous		
CC	recombination, (ii) 5' and 3' regulatory regions from plastid DNA linked		
CC	to a selectable marker gene, (iii) regulatory regions controlling a		
CC	foreign gene of interest, and (iv) at a cloning site for insertion of the		
CC	foreign gene adjacent to the marker gene. The method is used to transform		
CC	cruciferous plants, e.g. Brassica species. The combination of homologous		
CC	recombination, selectable marker and use of plastid regulatory sequences		
CC	improves generation of stably transformed plants. Expression of foreign		
CC	genes in plastids, rather than in the nucleus, avoids risk of		
CC	transmitting the foreign gene in the pollen, provides high levels of		
CC	protein expression, permits simultaneous incorporation of several genes		
CC	and avoids the positional effects and gene silencing associated with		
CC	nuclear transformation		
XX			
XX	Sequence 1417 BP; 312 A; 323 C; 379 G; 403 T; 0 U; 0 Other;		

Query Match 91.7%; Score 122; DB 2; Length 1417;  
Best Local Similarity 99.3%; Pred. No. 5.5e-33;  
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 GCTCCCCCGCCGCTTCATAGATGATGAAGGCTGTGGATTGACGTAGGGGG 60  
DB 23 GCTCCCCCGCCGCTTCATAGATGATGAAGGCTGTGGATTGACGTAGGGGG 82  
QY 61 CAGGATGAGCTATA-TTCTGGAGCGAATCTCCGGCGCAATACGAAGGCTTGATACAGT 119  
DB 83 CAGGATGAGCTATAATTCTCTGGAGCGAATCTCCGGCGCAATACGAAGGCTTGATACAGT 142  
QY 120 TGTAGGAGGAGATT 133  
DB 143 TGTAGGAGGAGATT 156  
RESULT 12  
ADE06203 standard; DNA; 1417 BP.  
AC ADE06203;  
XX  
DT 29-JUN-2004 (first entry)  
XX  
DE Plasmid targeting region of plasmid pGS85A.  
XX  
KM Vector; pZS391B; plasmid transformation; higher plant; transgene;  
KW Brassica plant; transplasmomic plant; DNA delivery; targeting region;  
KM plasmid pGS85A; ds.  
XX  
OS Unidentified.  
XX  
PN US2003200568-A1.  
XX  
PD 23-OCT-2003.  
XX  
PF 12-JUN-2003; 2003US-00460716.  
XX  
PR 06-MAR-1997; 97MO-US003444.  
PR 05-FEB-1999; 99US-00142114.  
PR 13-MAR-2000; 2000US-00524087.  
XX  
PA (MALI/) MALIGA P.  
PA (SKAR/) SKARJINSKAIA M.  
PA (MALI/) MALIGA Z S.  
PI Maliga P, Skarjinskaia M, Maliga ZS;  
XX  
DR WPI; 2003-852834/79.  
XX  
PT New improved vector for transforming plasmids of higher plants and  
PT comprising a targeting segment having first and second chimeric targeting  
PT sequences, useful for creating transplasmomic plants.  
XX  
PS Disclosure; SEQ ID NO 3; 35pp; English.  
XX  
CC The present invention relates to a new improved vector (pZS391B) for  
CC transforming plasmids of higher plants. The vector comprises a targeting  
CC segment having first and second chimeric targeting sequences for  
CC facilitating recombination within the plasmid genome, each of which  
CC flanks at least one transgene of interest and has a first portion derived  
CC from the plant species being targeted for transformation, and a second  
CC portion derived from a different plant species. The transgene constitutes  
CC a monocistronic or polycistronic expression unit comprising a selectable  
CC marker gene and a foreign gene of interest. It encodes a selectable  
CC marker, herbicide resistance or drought resistance gene. The selectable  
CC marker gene comprises kanamycin, streptomycin or spectinomycin. The  
CC plasmids are chloroplasts. The vector is useful for transforming plasmids  
CC of higher plants (e.g. Brassica plants), and for creating transplasmomic  
CC plants. The methods and compositions of the invention facilitate the  
CC regeneration of transformed plants following the delivery of beneficial  
CC DNA molecules. The present sequence represents the plasmid targeting

CC region of plasmid pGS85A.  
XX  
SQ Sequence 1417 BP; 312 A; 323 C; 379 G; 403 T; 0 U; 0 Other;  
QY Query Match 91.7%; Score 122; DB 10; Length 1417;  
Best Local Similarity 99.3%; Pred. No. 5.5e-33;  
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 GCTCCCCCGCCGCTTCATAGATGATGAAGGCTGTGGATTGACGTAGGGGG 60  
DB 23 GCTCCCCCGCCGCTTCATAGATGATGAAGGCTGTGGATTGACGTAGGGGG 82  
QY 61 CAGGATGAGCTATA-TTCTGGAGCGAATCTCCGGCGCAATACGAAGGCTTGATACAGT 119  
DB 83 CAGGATGAGCTATAATTCTCTGGAGCGAATCTCCGGCGCAATACGAAGGCTTGATACAGT 142  
QY 120 TGTAGGAGGAGATT 133  
DB 143 TGTAGGAGGAGATT 156  
RESULT 13  
ADM01283  
ID ADM01283 standard; DNA; 5834 BP.  
XX  
AC ADM01283;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Plasmid pVTPA DNA sequence.  
XX  
KM vector; plasmid; artificial intergene region; plant;  
KM transplasmomic angiosperm; agronomic property; stress resistance;  
KM rbcL gene; ds.  
XX  
OS Synthetic.  
XX  
PN WO2004029256-A2.  
XX  
PD 08-APR-2004.  
XX  
PF 15-SEP-2003; 2003WO-CY000009.  
XX  
PR 27-SEP-2002; 2002CU-00000208.  
XX  
PA (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.  
XX  
PI Selman-Housein Sosa G, Aguilar Cabeza E, Gonzalez Quintero ADC;  
PI Ramon Gonzalez O;  
XX  
DR WPI; 2004-316131/29.  
XX  
PT DNA vector for transformation and expression in plasmids, useful e.g. for  
PT producing pharmaceutical proteins or improving agronomic properties, has  
PT gene inserted in artificial intergene region.  
XX  
PS Example 1; SEQ ID NO 15; 74pp; Spanish.  
XX  
CC The invention relates to a DNA vector (A) for stable transformation and  
CC expression of genes (I) in plasmids, where (I) is inserted in an  
CC artificial intergene region (AIR) formed by combining two 5'-untranslated  
CC regions (5'-UTRs) of genes that transcribe in different directions and  
CC are derived from plants of different divisions or classes. (A) are used  
CC to produce transplasmomic angiosperms that have improved agronomic  
CC properties (e.g. resistance to biotic or abiotic stress) or express a  
CC very wide range of agricultural, veterinary, pharmaceutical, nutritional  
CC or industrial products, e.g. enzymes, vaccinating antigens, cytokines or  
CC immunoglobulins. Use of (A) eliminates the need for a transposon for gene  
CC insertion; inserted genes do not require promoters and terminators; and  
CC the structure of flanking sequences in (A) ensures universal  
CC applicability. Also any selection marker in (A) can be eliminated by  
CC homologous recombination. (A) provides efficient and stable expression of  
CC genes without causing any functional alterations. This sequence

CC represents an example of the vector of the invention.  
XX  
SQ Sequence 5834 BP; 1586 A; 1288 C; 1402 G; 1558 T; 0 U; 0 Other;  
Query Match 91.7%; Score 122; DB 12; Length 5834;  
Best Local Similarity 99.3%; Pred. No. 8.5e-33;  
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
1 GGTCCCCCGCGCTTCATAGATGATGATAGAGGCTCGTGGATTGACGTGAGGGG 60  
DB 1918 GCTCCCCCGCGCTTCATAGATGATGATAGAGGCTCGTGGATTGACGTGAGGGG 1977  
QY 61 CAGGATGGCTATA-TTCTGGAGGCGAACTCCGGCGAATACGAACGCTTGATACAT 119  
DB 1978 CAGGATGGCTATAATTCTGGAGGCGAACTCCGGCGAATACGAACGCTTGATACAT 2037  
QY 120 TGTAGGAGGAGATT 133  
DB 2038 TGTAGGAGGAGATT 2051

RESULT 14  
ADM01293  
ID ADM01293 standard; DNA; 6465 BP.  
XX  
AC ADM01293;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Plasmid pVTPA-Bar DNA sequence.  
XX  
XX vector; plasmid; artificial intergene region; plant;  
KM transplastomic angiosperm; agronomic property; stress resistance;  
KW rbcL gene; ds.  
XX  
OS Unidentified.  
XX  
PN WO2004029256-A2.  
XX  
PD 08-APR-2004.  
XX  
PF 15-SEP-2003; 2003WO-CU000009.  
XX  
PR 27-SEP-2002; 2002CU-00000208.  
XX  
PA (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.  
XX  
PI Selman-Housein Sosa G, Aguilar Cabeza E, Gonzalez Quintero ADC;  
PI Ramos Gonzalez O;  
XX  
DR WPI; 2004-316131/29.  
XX  
PT DNA vector for transformation and expression in plastids, useful e.g. for  
PT producing pharmaceutical proteins or improving agronomic properties, has  
PT gene inserted in artificial intergene region.  
XX  
PS Example 9; SEQ ID NO 25; 74pp; Spanish.

CC The invention relates to a DNA vector (A) for stable transformation and  
CC expression of genes (1) in plastids, where (1) is inserted in an  
CC artificial intergene region (AIR) formed by combining two 5'-untranslated  
CC regions (5'-UTRs) of genes that transcribe in different directions and  
CC are derived from plants of different divisions or classes. (A) are used  
CC to produce transplastomic angiosperms that have improved agronomic  
CC properties (e.g. resistance to biotic or abiotic stress) or express a  
CC very wide range of agricultural, veterinary, pharmaceutical, nutritional  
CC or industrial products, e.g. enzymes, vaccinating antigens, cytokines or  
CC immunoglobulins. Use of (A) eliminates the need for a transposon for gene  
CC insertion; inserted genes do not require promoters and terminators; and  
CC the structure of flanking sequences in (A) ensures universal  
CC applicability. Also any selection marker in (A) can be eliminated by  
CC homologous recombination. (A) provides efficient and stable expression of  
CC genes without causing any functional alterations. This sequence

CC represents the plasmid pVTPA-Bar, an example of the vector of the  
CC invention.  
XX  
SQ Sequence 6465 BP; 1705 A; 1503 C; 1602 G; 1655 T; 0 U; 0 Other;  
Query Match 91.7%; Score 122; DB 12; Length 6465;  
Best Local Similarity 99.3%; Pred. No. 8.8e-33;  
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
1 GGTCCCCCGCGCTTCATAGATGATGATAGAGGCTCGTGGATTGACGTGAGGGG 60  
DB 1918 GCTCCCCCGCGCTTCATAGATGATGATAGAGGCTCGTGGATTGACGTGAGGGG 1977  
QY 61 CAGGATGGCTATA-TTCTGGAGGCGAACTCCGGCGAATACGAACGCTTGATACAT 119  
DB 1978 CAGGATGGCTATAATTCTGGAGGCGAACTCCGGCGAATACGAACGCTTGATACAT 2037  
QY 120 TGTAGGAGGAGATT 133  
DB 2038 TGTAGGAGGAGATT 2051

RESULT 15  
ADM01290  
ID ADM01290 standard; DNA; 6659 BP.  
XX  
AC ADM01290;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Plasmid pVTPA-aada DNA sequence.  
XX  
XX vector; plasmid; artificial intergene region; plant;  
KM transplastomic angiosperm; agronomic property; stress resistance;  
KW rbcL gene; ds.  
XX  
OS Unidentified.  
XX  
PN WO2004029256-A2.  
XX  
PD 08-APR-2004.  
XX  
PF 15-SEP-2003; 2003WO-CU000009.  
XX  
PR 27-SEP-2002; 2002CU-00000208.  
XX  
PA (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.  
XX  
PI Selman-Housein Sosa G, Aguilar Cabeza E, Gonzalez Quintero ADC;  
PI Ramos Gonzalez O;  
XX  
DR WPI; 2004-316131/29.  
XX  
PT DNA vector for transformation and expression in plastids, useful e.g. for  
PT producing pharmaceutical proteins or improving agronomic properties, has  
PT gene inserted in artificial intergene region.  
XX  
PS Example 3; SEQ ID NO 22; 74pp; Spanish.

CC The invention relates to a DNA vector (A) for stable transformation and  
CC expression of genes (1) in plastids, where (1) is inserted in an  
CC artificial intergene region (AIR) formed by combining two 5'-untranslated  
CC regions (5'-UTRs) of genes that transcribe in different directions and  
CC are derived from plants of different divisions or classes. (A) are used  
CC to produce transplastomic angiosperms that have improved agronomic  
CC properties (e.g. resistance to biotic or abiotic stress) or express a  
CC very wide range of agricultural, veterinary, pharmaceutical, nutritional  
CC or industrial products, e.g. enzymes, vaccinating antigens, cytokines or  
CC immunoglobulins. Use of (A) eliminates the need for a transposon for gene  
CC insertion; inserted genes do not require promoters and terminators; and  
CC the structure of flanking sequences in (A) ensures universal  
CC applicability. Also any selection marker in (A) can be eliminated by  
CC homologous recombination. (A) provides efficient and stable expression of  
CC

CC genes without causing any functional alterations. This sequence  
CC represents the plasmid pVTPA-ada, an example of the vector of the  
CC invention.

XX  
SQ Sequence 6659 BP; 1790 A; 1490 C; 1636 G; 1743 T; 0 U; 0 Other;

Query Match 91.7%; Score 122; DB 12; Length 6659;  
Best Local Similarity 99.3%; Pred. No. 8.8e-33;  
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY	1	GCTCCCCCGCGCTTCATGATGAGATGATTAAGAGGCTCTGGGATTGACGTAGGGGG	60
DB	1918	GCTCCCCCGCGCTTCATGATGAGATGATTAAGAGGCTCTGGGATTGACGTAGGGGG	1977
QY	61	CAGGATGCTATA-TTCTGGAGCGAACTCCGGCGAATACGAAGCGCTTGATACAGT	119
DB	1978	CAGGATGCTATA-TTCTGGAGCGAACTCCGGCGAATACGAAGCGCTTGATACAGT	2037
QY	120	TGTAGGGAGGGGATT	133
DB	2038	TGTAGGGAGGGGATT	2051

Search completed: April 17, 2006, 23:45:51  
Job time : 487 secs

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OM nucleic - nucleic search, using sw model

Run on: April 17, 2006, 23:37:51 ; Search time 2233 Seconds  
(without alignments)  
3385.660 Million cell updates/sec

Title: US-10-663-241-32

Perfect score: 133  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_sts:\*  
11: gb\_sy:\*  
12: gb\_un:\*  
13: gb\_vl:\*  
14: gb\_hcg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	133	100.0	133	6	BD106711
2	133	100.0	133	6	AR403658
3	122	91.7	176	6	CO797808
4	122	91.7	1143	6	AR368829
5	122	91.7	1148	6	CO830289
6	122	91.7	1330	6	CO828070
7	122	91.7	1332	6	CO830287
8	122	91.7	1417	6	AR368830
9	122	91.7	3136	11	AF061065
10	122	91.7	4126	11	XXU12814
11	122	91.7	4126	11	XXU12815
12	122	91.7	4304	11	AY005806
13	122	91.7	5834	6	CO797809
14	122	91.7	6465	6	CO797819
15	122	91.7	6659	6	CO797816
16	122	91.7	7454	11	CTR312391
17	122	91.7	7549	6	CO797818
18	122	91.7	7626	11	CTR312392

c 19	122	91.7	7626	11	CTR312393	AJ312393 Chloropia
c 20	122	91.7	8483	11	AY895148	AY895148 Chloropia
c 21	122	91.7	9731	11	AY442171	AY442171 Chloropia
c 22	121	91.0	300	6	AR171710	AR171710 Sequence
c 23	121	91.0	300	6	AR171711	AR171711 Sequence
c 24	121	91.0	1183	6	BD235370	BD235370 Translatl
c 25	121	91.0	1327	6	CO828069	CO828069 Sequence
c 26	121	91.0	1613	6	CO830293	CO830293 Sequence
c 27	121	91.0	4508	11	AY575999	AY575999 Chloropia
c 28	121	91.0	4671	6	BD235379	BD235379 Translatl
c 29	117.8	88.6	4591	6	BD174931	BD174931 A system
c 30	114.8	86.3	142	6	BD174932	BD174932 A system
c 31	110	82.7	7039	11	DO073476	DO073476 Chloropia
c 32	107	80.5	119	15	CS001461	CS001461 Sequence
c 33	102.8	77.3	184	6	AR145914	AR145914 Sequence
c 34	102.8	77.3	201	6	AR242682	AR242682 Sequence
c 35	102.8	77.3	220	6	BD180933	BD180933 Method of
c 36	102.8	77.3	220	6	AX537601	AX537601 Sequence
c 37	102.8	77.3	2113	15	CHNT8N1	V00165 Tobacco chl
c 38	102.8	77.3	2962	11	XXU12809	U12809 Transformat
c 39	102.8	77.3	3019	11	XXU12810	U12810 Transformat
c 40	102.8	77.3	3019	11	XXU12811	U12811 Transformat
c 41	102.8	77.3	3274	15	CHNPT8NVT	X70938 N.Plumbagin
c 42	102.8	77.3	4174	11	XXU12812	U12812 Transformat
c 43	102.8	77.3	4363	6	AX798125	AX798125 Transformat
c 44	102.8	77.3	4363	6	AX798125	AX798125 Sequence
c 45	102.8	77.3	4363	6	AX798909	AX798909 Sequence

#### ALIGNMENTS

RESULT 1	BD106711	133 bp	DNA	linear	PAT 18-SEP-2002
LOCUS	BD106711				
DEFINITION	Plastid promoters for transgene expression in the plastids of higher plants.				
ACCESSION	BD106711	1	GI:23201529		
VERSION	BD106711.1				
KEYWORDS	JP 2002502262-A/32.				
SOURCE	JP 2002502262-A/32.				
ORGANISM	synthetic construct				
REFERENCE	other sequences; artificial sequences.				
AUTHORS	1 (bases 1 to 133)				
TITLE	Malliga, P., Silhavy, D. and Sriman, P.				
JOURNAL	Plastid promoters for transgene expression in the plastids of higher plants				
COMMENT	Patent: JP 2002502262-A 32 22-JAN-2002; RUTGERS THE STATE UNIVERSITY OF NEW JERSEY PN JP 2002502262-A/32				
	PD	22-JAN-2002			
	PF	03-JUN-1998	JP 1999502824		
	PR	03-JUN-1997	US 60/048376	12-SEP-1997	US 60/058670
	PAL	MALLIGA, DANIEL, SILHAVY, PRIYA SRIRAMAN			
	PC	C12N15/04, C12N15/00, C12N15/09, C12N15/29, C12N15/82, A01H1/00, PC			
	A01H3/00,				
	PC	A01H5/00			
	CC	Strandedness: Single;			
	FH	Key	Location/Qualifiers.		
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	/db_xref="taxon:32630"				
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Best Local Similarity	100.0%; Pred. No. 1e-33;				
Matches	133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 GCTCCCGCCGCTCTTCAATGAGATGATGATGAGGCTGTGGATTGACGTAGGGGG 60				
DB	1 GCTCCCGCCGCTCTTCAATGAGATGATGATGAGGCTGTGGATTGACGTAGGGGG 60				

OY		61 CAGGGATGGCTTATTTCGTGGGACCACTCCGGGGGAATAAGAACCGTTGGATCACTT	120
Dd		61 CAGGGATGGCTAATATTCGTGGGACCACTCCGGGGGAATAAGAACCGTTGGATCACTT	120
OY		121 GTAGGAGGAGGATT	133
Dd		121 GTAGGAGGAGGATT	133
RESULT 2			
LOCUS	AR403658	133 bp	DNA
DEFINITION	Sequence 32 from patent US 6624296.		linear PAT 18-DEC-2003
ACCESSION	AR403658		
VERSION	AR403658.1 GI:40151276		
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 133)		
TITLE	Majiga,P., Silhavy,D. and Sritaman,P. Plasid promoters for transgene expression in the plactids of higher plants Patent: US 6624296-A 32 23-SEP-2003; Rutgers, The State University of New Jersey; East Brunswick, NJ		
JOURNAL			
FEATURES			
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ORIGIN			
Query Match	100.0%; Score 133; DB 6; Length 133;		
Best Local Similarity	100.0%; Pred. No. 1e-33; Mismatches 0; Indels 0; Gaps 0;		
Matches 133; Conservative 0;			
OY		1 GCTCCCCCGCGCTCGTTCATAGATGGATTAAGAAGCTCGTGAGATTGACGTGAGGGG	60
Dd		1 GCTCCCCCGCGCTCGTTCATAGATGGATTAAGAAGCTCGTGAGATTGACGTGAGGGG	60
OY		61 CAGGATGGCTTATTTCGTGGGACCACTCCGGGGGAATACGAACGCTTGGATCAGTT	120
Dd		61 CAGGATGGCTAATATTCGTGGGACCACTCCGGGGGAATACGAACGCTTGGATCAGTT	120
OY		121 GTAGGAGGAGGATT	133
Dd		121 GTAGGAGGAGGATT	133
RESULT 3			
LOCUS	CQ797808	176 bp	DNA
DEFINITION	Sequence 14 from Patent WO2004029256.		linear PAT 20-APR-2004
ACCESSION	CQ797808		
VERSION	CQ797808.1 GI:46426081		
KEYWORDS	.		
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	other sequences; artificial sequences.		
AUTHORS	1 Belman-housein Sosa,G., aguiar Cabeza,E., gonz lez Quintero,A.D. and ramos gonz lez,O. Vector for the production of transplastomic angiosperm plants Patent: WO 2004029256-A 14 08-APR-2004; CENTRO DE INGENIERIA GENETICA Y BIOTECNOLOGIA (CU) Location/Qualifiers		
TITLE			
JOURNAL			
FEATURES			
source	1..176 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Description of Artificial Sequence: Synthetic DNA fragment codifying for the promoter region of the plasid 16S ribosomal RNA (Prrn), with added restriction sites."		

Query Match	91.7%	Score 122	DB 6	Length 176
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Qy	1	GCTCCCCCGCGCTTCATATGAGAAATGATTAAGAGGCTCGTGGATTGACGTAGGGGG	60	
Db	16	GCTCCCCCGCGCTTCATATGAGAAATGATTAAGAGGCTCGTGGATTGACGTAGGGGG	75	
Qy	61	CAGGATGGCTATA-TTCTGGAGCGAATCTCCGGCGAATACGAACGCTTGTATACGT	119	
Db	76	CAGGATGGCTATA-TTCTGGAGCGAATCTCCGGCGAATACGAACGCTTGTATACGT	135	
Qy	120	TGTAGGAGGGGATT 133		
Db	136	TGTAGGAGGGGATT 149		
RESULT 4				
AR368829/c				
LOCUS	AR368829	1143 bp	DNA	linear PAT 12-SEP-2003
DEFINITION	Sequence 6 from patent US 6376744.			
ACCESSION	AR368829			
VERSION	AR368829.1	GI:34603191		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 1143)			
TITLE	Maliga, P., Sikdar, S. and Reddy, S. V.			
JOURNAL	Plastid transformation in Arabidopsis thaliana			
FEATURES	Patent: US 6376744-A 6 23-APR-2002;			
source	Rutgers, The State University of New Jersey; New Brunswick, NJ			
	Location/Qualifiers			
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Qy	1	GCTCCCCCGCGCTTCATATGAGAAATGATTAAGAGGCTCGTGGATTGACGTAGGGGG	60	
Db	1130	GCTCCCCCGCGCTTCATATGAGAAATGATTAAGAGGCTCGTGGATTGACGTAGGGGG	1071	
Qy	61	CAGGATGGCTATA-TTCTGGAGCGAATCTCCGGCGAATACGAACGCTTGTATACGT	119	
Db	1070	CAGGATGGCTATA-TTCTGGAGCGAATCTCCGGCGAATACGAACGCTTGTATACGT	1011	
Qy	120	TGTAGGAGGGGATT 133		
Db	1010	TGTAGGAGGGGATT 997		
RESULT 5				
CQ830289				
LOCUS	CQ830289	1148 bp	DNA	linear PAT 12-JUL-2004
DEFINITION	Sequence 3 from Patent WO2004055191.			
ACCESSION	CQ830289			
VERSION	CQ830289.1	GI:50250782		
KEYWORDS				
SOURCE	synthetic construct			
ORGANISM	synthetic construct			
REFERENCE	other sequences; artificial sequences.			
AUTHORS	1			
TITLE	Tiesot, G., Wisniewski, J.P. and Penillo, J.M.			
JOURNAL	Expression of hydroxyphenylpyruvate dioxygenase in plasmids of plants for herbicide tolerance			
	Patent: WO 2004055191-A 3 01-JUL-2004;			
	Biogenma (FR)			



misc_feature	complement(1059..2201)	/note="chimeric aada gene in a tobacco plasmid expression cassette"
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promoter	complement(2054..2188)	/note="Chimeric promoter based on the promoter of the RRNA operon"
misc_feature	/c1c1ation=[1]	2193..2198
misc_feature	/note="KpnI cloning site"	2202..3136
misc_feature	/note="Arabidopsis thaliana plasmid DNA"	
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Query Match	91.7%; Score 122; DB 11; Length 3136;	
Best Local Similarity	99.3%; Pred. No. 6,3e-30;	
Matches 133; Conservative	0; Mismatches 0; Indels 1; Gaps 1;	
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QY	61 CAGGAGATGCGATAT-TTCTGGAGAGCAACTCCGGGCGAATACGAAGCGCTTGATACAGT	119
DB	2128 CAGGAGATGCGATATTTCTGGAGAGCAACTCCGGGCGAATACGAAGCGCTTGATACAGT	2065
QY	120 TGTAGGAGAGGATT 133	
DB	2068 TGTAGGAGAGGATT 2055	
RESULT 10		
LOCUS	XXU12814/c	
DEFINITION	XXU12814	4126 bp DNA linear SYN 24-MAY-1995
ACCESSION	U12814	
VERSION	U12814.1	GI:559552
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
FEATURES		
source		

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1. 1949  
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region, Genbank Accession Number Z00044"  
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AKRELQFGEWQNDILAGI.FEPATIDIDIALITLTKAREHSVALVGPAAELPDPVLEQ  
DLEALNSTLTLMNSPPDWAGDERNVVLTLSIWSAVYGLAPKDVADAMMERLPA  
QYQPVILBARQAVLQGEEDRLASRADQLEEFVHYVKGITKVVGK"  
2894..2950  
/note="multiple cloning site: EcoRI, SacI, KpnI, SmaI,  
XbaI, SalI, PstI, HindIII"  
2951..4126  
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region, Genbank Accession Number Z00044"

## ORIGIN

Query Match 91.7%; Score 122; DB 11; Length 4126;  
Best Local Similarity 99.3%; Pred. No. 6.4e-30;  
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGTCCCCCGCGCTGCTCAATGAGATGATGAGAGCTCGTGGATTGACGGAGGGGG 60  
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Db 2888 GGTCCCCCGCGCTGCTCAATGAGATGAGATGAGAGCTCGTGGATTGACGGAGGGGG 2829  
QY 61 CAGGATGGCTATA-TTCTGGAGCGAACTCCGGCGAATACGAAGCGCTTGATCACT 119  
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Db 2828 CAGGATGGCTATA-TTCTGGAGCGAACTCCGGCGAATACGAAGCGCTTGATCACT 2769  
QY 120 TGTAGGAGGGATT 133  
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Db 2768 TGTAGGAGGGATT 2755

## RESULT 11

XXU12815/c

LOCUS XXU12815 4126 bp DNA linear SYN 24-MAY-1995  
DEFINITION Transformation vector pPRV112B, plasmid targeting segment.  
ACCESSION U12815  
VERSION U12815.1 GI:559554

## KEYWORDS

SOURCE Cloning vector pPRV112B  
ORGANISM Cloning vector pPRV112B  
OTHER SEQUENCES; artificial sequences; vectors.

## REFERENCE

1 (bases 1 to 4126)  
Zoubenko,O.V., Allison,L.A., Svab,Z. and Maliga,P.  
Efficient targeting of foreign genes into the tobacco plastid  
genome

JOURNAL Nucleic Acids Res. 22 (19), 3819-3824 (1994)

## PUBMED

7937099

2 (bases 1 to 4126)  
Hajdukiewicz,P.T.  
Direct Submission

## JOURNAL

Submitted (01-AUG-1994) Peter T. Hajdukiewicz, Wakeman Inst.,  
Rutgers University, Old Hoes Lane, Piscataway, NJ 08855, USA

## FEATURES

## source

Location/Qualifiers  
1. 4126  
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DLEALNSTLTLMNSPPDWAGDERNVVLTLSIWSAVYGLAPKDVADAMMERLPA  
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## misc\_feature

## RNA

## misc\_feature

## gene

## trnA

## gene

## CDS

## ORIGIN

Query Match 91.7%; Score 122; DB 11; Length 4126;  
Best Local Similarity 99.3%; Pred. No. 6.4e-30;  
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGTCCCCCGCGCTGCTCAATGAGATGATGAGAGCTCGTGGATTGACGGAGGGGG 60  
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QY 61 CAGGATGGCTATA-TTCTGGAGCGAACTCCGGCGAATACGAAGCGCTTGATCACT 119  
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Db 2828 CAGGATGGCTATA-TTCTGGAGCGAACTCCGGCGAATACGAAGCGCTTGATCACT 2769  
QY 120 TGTAGGAGGGATT 133  
|||||  
Db 2768 TGTAGGAGGGATT 2755

## RESULT 12

AY005806/c

LOCUS AY005806 4304 bp DNA linear SYN 28-JAN-2002  
DEFINITION Transformation vector pUT554, plasmid targeting region.  
ACCESSION AY005806  
VERSION AY005806.1 GI:10442803

## KEYWORDS

SOURCE synthetic construct  
ORGANISM synthetic construct  
OTHER SEQUENCES; artificial sequences.

## REFERENCE

1 (bases 1 to 4304)  
Suzuki,J.Y. and Maliga,P.  
Engineering of the rpl23 gene cluster to replace the plastid RNA  
polymerase alpha subunit with the Escherichia coli homologue

## JOURNAL

CURR. GENET.

38 (4), 218-225 (2000)  
2 (bases 1 to 4304)

AUTHORS

Suzuki, J.Y. and Maliga, P.  
Direct Submission  
Submitted (26-JUL-2000) Waksman Institute, Rutgers University, 190  
Frelinghuysen Road, Piscataway, NJ 08854, USA

FEATURES

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PMRYPAKRELPGEWQRNDIAGIFEPATPIDALITLTKAREHSAVALGVAAEELPD  
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2637..4304  
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SRNLIDILFIPLHMEEDNLYLQDQHTVLPSPFHDKLAKLTKKKLAIKSLIFIDQ  
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ORIGIN

Query Match 91.7%; Score 122; DB 11; Length 4304;  
Best Local Similarity 99.3%; Pred. No. 6.4e-30;  
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGCTTCATGAGATGATAGAGGCTCGTGGATTGACGTGAGGGG 60  
DB 2604 GCTCCCCCGCGCTTCATGAGATGATAGAGGCTCGTGGATTGACGTGAGGGG 2545  
QY 61 CAGGATGGCTATTA-TTCTGGAGACCGAATCCGGCCGAATACGAAGCGCTTGATACGT 119  
DB 2544 CAGGATGGCTATTA-TTCTGGAGACCGAATCCGGCCGAATACGAAGCGCTTGATACGT 2485  
QY 120 TGTAGGAGGAGGATT 133  
DB 2484 TGTAGGAGGAGGATT 2471

RESULT 13  
LOCUS CQ797809 5834 bp DNA linear PAT 20-APR-2004  
DEFINITION Sequence 15 from Patent WO2004029256.  
ACCESSION CQ797809  
VERSION CQ797809.1 GI:46426082  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1

AUTHORS selman-housein Sosa,G., aguiar Cabeza,E., gonz lez Quintero,A.D.  
and ramos gonz lez,O.  
TITLE Vector for the production of transplastomic angiosperm plants  
JOURNAL Patent: WO 2004029256-A 15 08-APR-2004;

FEATURES  
source  
Location/Qualifiers  
1. 5834  
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sequence of DNA fragment from the vector pVTPA between the  
rice atpb and tobacco rbcl borders."

## ORIGIN

Query Match 91.7%; Score 122; DB 6; Length 5834;  
Best Local Similarity 99.3%; Pred. No. 6.5e-30;

Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGCTTCATAGATGAGATGAGAGGCTCGTGGATTGACGTGAGGGG 60  
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DB 1918 GCTCCCCCGCGCTTCATAGATGAGATGAGAGGCTCGTGGATTGACGTGAGGGG 1977  
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QY 61 CAGGATGGCTATA-TTCTGGAGCGCAACTCCGGCGAATACGAGCGCTTGATACAGT 119  
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DB 1978 CAGGATGGCTATA-TTCTGGAGCGCAACTCCGGCGAATACGAGCGCTTGATACAGT 2037  
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QY 120 TGTAGGAGGAGATT 133  
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DB 2038 TGTAGGAGGAGATT 2051  
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## RESULT 14

CO797819 6465 bp DNA linear PAT 20-APR-2004  
LOCUS CQ797819  
DEFINITION Sequence 25 from Patent WO2004029256.  
ACCESSION CQ797819  
VERSION CQ797819.1 GI:46426092  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.

REFERENCE  
1 selman-housein Sosa,G., aguiar Cabeza,E., gonz lez Quintero,A.D.  
and ramos gonz lez,O.  
TITLE Vector for the production of transplastomic angiosperm plants  
JOURNAL Patent: WO 2004029256-A 25 08-APR-2004;

FEATURES  
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Location/Qualifiers  
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the rice atpb and tobacco rbcl borders."

## ORIGIN

Query Match 91.7%; Score 122; DB 6; Length 6465;  
Best Local Similarity 99.3%; Pred. No. 6.5e-30;

Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 120 TGTAGGAGGAGATT 133  
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DB 2038 TGTAGGAGGAGATT 2051  
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## RESULT 15

CO797816 6659 bp DNA linear PAT 20-APR-2004  
LOCUS CQ797816  
DEFINITION Sequence 22 from Patent WO2004029256.  
ACCESSION CQ797816  
VERSION CQ797816.1 GI:46426089  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.

## REFERENCE

1 selman-housein Sosa,G., aguiar Cabeza,E., gonz lez Quintero,A.D.  
and ramos gonz lez,O.  
TITLE Vector for the production of transplastomic angiosperm plants  
JOURNAL Patent: WO 2004029256-A 22 08-APR-2004;

FEATURES  
source  
Location/Qualifiers  
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## ORIGIN

Query Match 91.7%; Score 122; DB 6; Length 6659;  
Best Local Similarity 99.3%; Pred. No. 6.5e-30;

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QY 61 CAGGATGGCTATA-TTCTGGAGCGCAACTCCGGCGAATACGAGCGCTTGATACAGT 119  
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DB 1978 CAGGATGGCTATA-TTCTGGAGCGCAACTCCGGCGAATACGAGCGCTTGATACAGT 2037  
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QY 120 TGTAGGAGGAGATT 133  
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DB 2038 TGTAGGAGGAGATT 2051  
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